

OM protein - protein search, using sw model

Run on: March 4, 2004, 15:21:50 ; Search time 82.0638 Seconds
(without alignments)
1397.867 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
Perfect score: 2113
Sequence: 1 ALEPALASPAGAANFLAMVD.....STEDVASNCVPAQSLSEPIL 406

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2113	100.0	413	4	AAE10658	Aae10658 Acid-proc
2	2113	100.0	413	4	AAE02610	Aae02610 Human aci
3	2113	100.0	413	5	ABB78619	Abb78619 Asp-1delt
4	2113	100.0	475	4	AAE10657	Aae10657 Secreted
5	2113	100.0	475	4	AAE02609	Aae02609 Human sec
6	2113	100.0	475	5	ABB78618	Abb78618 Secreted
7	2113	100.0	481	4	AAG75592	Aag75592 Human col
8	2113	100.0	518	2	AAW61362	Aaw61362 Aspartic
9	2113	100.0	518	2	AAV13799	Aay13799 Human asp

10	2113	100.0	518	2	AAAY22239	Aay22239	Human	CSP
11	2113	100.0	518	2	AAAY41714	Aay41714	Human	PRO
12	2113	100.0	518	3	AAAY88424	Aay88424	Human	asp
13	2113	100.0	518	3	AAB44270	Aab44270	Human	PRO
14	2113	100.0	518	4	AAU07201	Aau07201	Human	asp
15	2113	100.0	518	4	AAE10628	Aae10628	Human	asp
16	2113	100.0	518	4	AAE10656	Aae10656	Human	Asp
17	2113	100.0	518	4	AAE06858	Aae06858	Human	asp
18	2113	100.0	518	4	AAE02608	Aae02608	Human	Asp
19	2113	100.0	518	4	AAE02580	Aae02580	Human	asp
20	2113	100.0	518	4	AAU29059	Aau29059	Human	PRO
21	2113	100.0	518	4	AAU06602	Aau06602	Human	Asp
22	2113	100.0	518	5	ABB06531	Abb06531	Human	asp
23	2113	100.0	518	5	ABB78589	Abb78589	Human	Asp
24	2113	100.0	518	5	ABB78617	Abb78617	Human	Asp
25	2113	100.0	518	5	ABB07453	Abb07453	Human	BAC
26	2113	100.0	518	6	ABU58435	Abu58435	Human	PRO
27	2113	100.0	518	6	ABU87983	Abu87983	Novel	hum
28	2113	100.0	518	6	ABU84298	Abu84298	Human	sec
29	2113	100.0	518	6	ABR66172	Abr66172	Human	sec
30	2113	100.0	518	6	ABR65562	Abr65562	Human	sec
31	2113	100.0	518	6	ABU99502	Abu99502	Human	sec
32	2113	100.0	518	6	ABU82741	Abu82741	Human	PRO
33	2113	100.0	518	6	ABU89862	Abu89862	Novel	hum
34	2113	100.0	518	6	ABR68111	Abr68111	Human	sec
35	2113	100.0	518	6	ABU96164	Abu96164	Novel	hum
36	2113	100.0	518	6	ABU92595	Abu92595	Human	sec
37	2113	100.0	518	6	ABO08672	Abo08672	Human	sec
38	2113	100.0	518	6	ABO02724	Abo02724	Human	sec
39	2113	100.0	518	6	ABR74878	Abr74878	Human	sec
40	2113	100.0	518	6	ABR94640	Abr94640	Human	sec
41	2113	100.0	518	6	ABO25216	Abo25216	Novel	hum
42	2113	100.0	518	6	ABU85613	Abu85613	Human	PRO
43	2113	100.0	518	6	ABU98773	Abu98773	Novel	hum
44	2113	100.0	518	6	ABU97988	Abu97988	Novel	hum
45	2113	100.0	518	6	ABU91694	Abu91694	Novel	hum

ALIGNMENTS

RESULT 1

AAE10658

ID AAE10658 standard; protein; 413 AA.

XX

AC AAE10658;

XX

DT 10-DEC-2001 (first entry)

XX

DE Acid-processed hu-Asp 1 lacking TM domain and containing (His)6 tag.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.

XX

OS Homo sapiens.

OS Synthetic.

XX
 PN GB2357767-A.
 XX
 PD 04-JUL-2001.
 XX
 PF 22-SEP-2000; 2000GB-00023315.
 XX
 PR 23-SEP-1999; 99US-00404133.
 PR 23-SEP-1999; 99US-0155493P.
 PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2001-444208/48.
 XX
 PT Polypeptide comprising fragments of human aspartyl protease with amyloid
 PT precursor protein processing activity and alpha-secretase activity, for
 PT identifying modulators useful in treating Alzheimer's disease.
 XX
 PS Example 14; Page 158; 187pp; English.
 XX
 CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
 CC proteins which lack transmembrane domain or amino terminal domain or
 CC cytoplasmic domain and retains alpha-secretase activity and amyloid
 CC protein precursor (APP) processing activity. The proteins of the
 CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
 CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
 CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
 CC are useful for treating Alzheimer's disease (AD) which causes progressive
 CC dementia with consequent formation of amyloid plaques, neurofibrillary
 CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
 CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
 CC with the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is the acid- processed
 CC form of human Asp 1 protein lacking a transmembrane (TM) domain and
 CC containing (His)6 tag
 XX
 SQ Sequence 413 AA;

Query Match 100.0%; Score 2113; DB 4; Length 413;
 Best Local Similarity 100.0%; Pred. No. 1.5e-198;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	1	ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Qy	61	HSYIDTYFDTERSSTYRSKGFDTVKYTGGSWTGFVGEDLV TIPKGFNTSFLVNIATIFE	120
Db	61	HSYIDTYFDTERSSTYRSKGFDTVKYTGGSWTGFVGEDLV TIPKGFNTSFLVNIATIFE	120
Qy	121	SEFFFLPGIKWNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPVAGS	180

Db	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
QY	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
QY	241	DSGTTLLRLRPQKVFD AVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	300
Db	241	DSGTTLLRLRPQKVFD AVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	300
QY	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
QY	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406

RESULT 2

AAE02610

ID AAE02610 standard; protein; 413 AA.
 XX
 AC AAE02610;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Human acid-processed form of aspartyl protease-1 deltaTM (His)6 protein.
 XX
 KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
 KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl;
 KW beta-secretase; acid-processed Asp-1 deltaTM (His)6 protein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200123533-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 22-SEP-2000; 2000WO-US026080.
 XX
 PR 23-SEP-1999; 99US-0155493P.
 PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Gurney M, Bienkowski MJ;
 XX
 DR WPI; 2001-290516/30.
 XX
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease.
 XX
 PS Example 14; Page 186-187; 189pp; English.

XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human acid-processed form of
CC Aspartyl protease-1 (Asp-1) deltaTM (His)6 protein which is used for the
CC expression of pre-pro-human-Aspartyl protease 1 (Asp1). The protein is
CC obtained by replacing C-terminal transmembrane and cytoplasmic domains
CC with a hexahistidine purification tag in the human Aspartyl protease 1
XX
SQ Sequence 413 AA;

Query Match 100.0%; Score 2113; DB 4; Length 413;
Best Local Similarity 100.0%; Pred. No. 1.5e-198;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
      |||
Db      1 ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60

QY     61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATIFE 120
      |||
Db     61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATIFE 120

QY    121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
      |||
Db    121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180

QY    181 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 240
      |||
Db    181 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 240

QY    241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
      |||
Db    241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300

QY    301 RDENSSRSFRITILPQLYIQPMGAGLNYECYREGISPSTNALVIGATVMEGFYVIFDRA 360
      |||
Db    301 RDENSSRSFRITILPQLYIQPMGAGLNYECYREGISPSTNALVIGATVMEGFYVIFDRA 360

QY    361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
      |||
Db    361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
```

RESULT 3

ABB78619

ID ABB78619 standard; protein; 413 AA.

XX

AC ABB78619;

XX

DT 16-JUL-2002 (first entry)

XX

DE Asp-1deltaTM(his)6 acid-processed form SEQ ID NO:68.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
 KW chromosome 21.
 XX
 OS Homo sapiens.
 XX
 PN GB2367060-A.
 XX
 PD 27-MAR-2002.
 XX
 PF 29-OCT-2001; 2001GB-00025934.
 XX
 PR 23-SEP-1999; 99US-00404133.
 PR 23-SEP-1999; 99US-0155493P.
 PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 PR 22-SEP-2000; 2000GB-00023315.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2002-397167/43.
 XX
 PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
 PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
 XX
 PS Example 14; Page 158-159; 182pp; English.
 XX
 CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the non
 CC -coding strand complementary to a defined 1804 nucleotide sequence (see
 CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
 CC proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain); (3) a purified polynucleotide (III') comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or
 CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
 CC substrate (I) may be used as an enzyme substrate in assays to detect
 CC aspartyl protease activity, (II) and therefore diagnose diseases
 CC associated with aberrant hu-Asp1 expression and activity such as
 CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 CC sequence represents the Asp-1deltaTM(his)6 acid-processed form amino acid
 CC sequence, which is used in an example from the present invention
 XX
 SQ Sequence 413 AA;

Query Match

100.0%; Score 2113; DB 5; Length 413;

Best Local Similarity 100.0%; Pred. No. 1.5e-198;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
      |||
Db      1 ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60

QY     61 HSYIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
      |||
Db     61 HSYIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120

QY    121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
      |||
Db    121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180

QY    181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 240
      |||
Db    181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 240

QY    241 DSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL 300
      |||
Db    241 DSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL 300

QY    301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
      |||
Db    301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360

QY    361 QKRVGFAASPCA EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI L 406
      |||
Db    361 QKRVGFAASPCA EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI L 406
```

RESULT 4

AAE10657

ID AAE10657 standard; protein; 475 AA.

XX

AC AAE10657;

XX

DT 10-DEC-2001 (first entry)

XX

DE Secreted recombinant hu-Asp 1 with (His)6 tag and lacking TM domain.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN GB2357767-A.

XX

PD 04-JUL-2001.

XX

PF 22-SEP-2000; 2000GB-00023315.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2001-444208/48.
 XX
 PT Polypeptide comprising fragments of human aspartyl protease with amyloid
 PT precursor protein processing activity and alpha-secretase activity, for
 PT identifying modulators useful in treating Alzheimer's disease.
 XX
 PS Example 14; Page 156-158; 187pp; English.
 XX
 CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
 CC proteins which lack transmembrane domain or amino terminal domain or
 CC cytoplasmic domain and retains alpha-secretase activity and amyloid
 CC protein precursor (APP) processing activity. The proteins of the
 CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
 CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
 CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
 CC are useful for treating Alzheimer's disease (AD) which causes progressive
 CC dementia with consequent formation of amyloid plaques, neurofibrillary
 CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
 CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
 CC with the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is secreted
 CC recombinant human Asp 1 protein lacking a transmembrane (TM) domain and
 CC containing a (His)6 tag. This sequence is generated from human Asp 1
 CC protein by the deletion of its C-terminal TM domain and addition of hexa-
 CC histidine tag at its C-terminus
 XX
 SQ Sequence 475 AA;

Query Match 100.0%; Score 2113; DB 4; Length 475;
 Best Local Similarity 100.0%; Pred. No. 1.9e-198;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ALEPALASPAGAAANFLAMVDNLQDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
QY	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
QY	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
QY	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	302
QY	241	DSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIIYL	300

Db	303	DSGTTLLRLPQKVFD	AVVEAVARASLIPEFSDGFWTGSQ	LACWTNSETPWSYFPKIS	IYL 362
QY	301	RDENSSRSFRITILPQ	LYIQPMMGAGLNYECYRFGIS	PSTNALVIGATVMEGFYVIF	DRA 360
Db	363	RDENSSRSFRITILPQ	LYIQPMMGAGLNYECYRFGIS	PSTNALVIGATVMEGFYVIF	DRA 422
QY	361	QKRVGFAASPCA	EIAGAAVSEISGPFSTEDVA	SNCVPAQSLSEPI	L 406
Db	423	QKRVGFAASPCA	EIAGAAVSEISGPFSTEDVA	SNCVPAQSLSEPI	L 468

RESULT 5

AAE02609

ID AAE02609 standard; protein; 475 AA.

XX

AC AAE02609;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human secreted aspartyl protease-1 (Asp-1) deltaTM (His)6 protein.

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;

KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl;

KW beta-secretase; secreted Asp-1 deltaTM (His)6 protein.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US026080.

XX

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney M, Bienkowski MJ;

XX

DR WPI; 2001-290516/30.

XX

PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.

XX

PS Example 14; Page 184-186; 189pp; English.

XX

CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human secreted recombinant

CC Aspartyl protease-1 (Asp-1) deltaTM (His)6 protein which is used for the
CC expression of pre-pro-human-Aspartyl protease 1 (Asp1). The protein is
CC obtained by replacing C-terminal transmembrane and cytoplasmic domains
CC with a hexahistidine purification tag in the human Aspartyl protease 1
XX
SQ Sequence 475 AA;

Query Match 100.0%; Score 2113; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-198;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

QY      61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

QY     121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 242

QY     181 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 302

QY     241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     303 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 362

QY     301 RDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     363 RDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

QY     361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468
```

RESULT 6

ABB78618

ID ABB78618 standard; protein; 475 AA.

XX

AC ABB78618;

XX

DT 16-JUL-2002 (first entry)

XX

DE Secreted recombinant Asp-1deltaTM(his)6 amino acid SEQ ID NO:67.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW chromosome 21.

XX

OS Homo sapiens.

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-00025934.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
PR 22-SEP-2000; 2000GB-00023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowski MJ, Gurney M;
XX
DR WPI; 2002-397167/43.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS Example 14; Page 156-158; 182pp; English.
XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents a secreted recombinant Asp-1deltaTM(his)6 amino acid
CC sequence, which is used in an example from the present invention
XX
SQ Sequence 475 AA;

QY 1 ALEPALASPAGAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
 |||
 Db 63 ALEPALASPAGAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

QY	61	HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
QY	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
QY	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	302
QY	241	DSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL	300
Db	303	DSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL	362
QY	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
QY	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 7

AAG75592

ID AAG75592 standard; protein; 481 AA.
 XX
 AC AAG75592;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen protein SEQ ID NO:6356.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; chromosome 21.
 XX
 OS Homo sapiens.
 XX
 PN WO200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-US026524.
 XX
 PR 29-SEP-1999; 99US-0157137P.
 PR 03-NOV-1999; 99US-0163280P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX
 DR WPI; 2001-235357/24.
 DR N-PSDB; AAH34997.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,

RESULT 8
 AAW61362
 ID AAW61362 standard; protein; 518 AA.
 XX
 AC AAW61362;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-SEP-1998 (first entry)
 XX
 DE Aspartic proteinase ASP1.
 XX
 KW ASP1; Aspartic proteinase; Alzheimer's disease; cancer; melanoma.
 XX
 OS Homo sapiens.
 XX
 PN EP848062-A2.
 XX
 PD 17-JUN-1998.
 XX
 PF 01-DEC-1997; 97EP-00309648.
 XX
 PR 14-DEC-1996; 96GB-00026022.
 PR 06-OCT-1997; 97US-00999723.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Powell DJ, Southan C, Chapman CG, Evans JR;
 XX
 DR WPI; 1998-314477/28.
 DR N-PSDB; AAV27962.
 XX
 PT New isolated polynucleotide encodes Aspartic protease polypeptide - used
 PT to diagnosis, treat and vaccinate against Alzheimer's disease, cancer and
 PT melanoma.
 XX
 PS Claim 11; Page 7; 19pp; English.
 XX
 CC The human ASP1 protein is structurally related to other proteins of the
 CC Aspartic proteinase family. ASP 1 polypeptides and polynucleotides can be
 CC used to diagnosis, treat and vaccinate against Alzheimer's disease,
 CC cancer and melanoma. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2113; DB 2; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2.2e-198;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
Qy	61	HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIATIFE	182

QY	121	SENFFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
QY	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	302
QY	241	DSGTTLLRLRPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	300
Db	303	DSGTTLLRLRPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	362
QY	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
QY	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 9

AAY13799

ID AAY13799 standard; protein; 518 AA.
 XX
 AC AAY13799;
 XX
 DT 21-SEP-1999 (first entry)
 XX
 DE Human aspartyl protease, CSP56.
 XX
 KW CSP56; human; aspartyl protease; diagnosis; neoplasia; tumour;
 KW breast tumour; colon tumour.
 XX
 OS Homo sapiens.
 XX
 PN W09933963-A1.
 XX
 PD 08-JUL-1999.
 XX
 PF 14-DEC-1998; 98WO-US026547.
 XX
 PR 31-DEC-1997; 97US-0070112P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Giese KW, Xin H;
 XX
 DR WPI; 1999-430240/36.
 DR N-PSDB; AAX89297.
 XX
 PT Human CSP56 protein for diagnosis of neoplasia.
 XX
 PS Claim 2; Fig 2A; 5lpp; English.
 XX
 CC This represents a human CSP56 protein, a novel aspartyl protease. The

CC CSP56 protein can be used in methods for diagnosing neoplasia, for
CC determining the metastatic potential of a tumour, and for screening test
CC compounds for the ability to suppress the metastatic potential of a
CC tumour. The tumours are preferably from breast or colon
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 2113; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.2e-198;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
Qy	61	HSYIDTYFDTERSSTYRSKGFDTVKYTGGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTGGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
Qy	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS	242
Qy	181	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	302
Qy	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	362
Qy	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
Qy	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 10

AAY22239

ID AAY22239 standard; protein; 518 AA.

XX

AC AAY22239;

XX

DT 20-SEP-1999 (first entry)

XX

DE Human CSP56, aspartyl-type protease, protein sequence.

XX

KW Metastatic marker protein; human; cancer metastasis; breast cancer;
KW colon cancer; diagnosis; therapy; tumour; metastatic potential; CSP56;
KW aspartyl-type protease.

XX

OS Homo sapiens.

XX

PN WO9934004-A2.

XX
 PD 08-JUL-1999.
 XX
 PF 24-DEC-1998; 98WO-US027608.
 XX
 PR 31-DEC-1997; 97US-0070112P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Xin H, Giese K;
 XX
 DR WPI; 1999-430248/36.
 DR N-PSDB; AAX84708.
 XX
 PT New polynucleotides associated with cancer metastasis.
 XX
 PS Claim 4; Page 78-80; 80pp; English.
 XX
 CC This sequence represents a polypeptide of the invention, and is an
 CC aspartyl-type protease, designated CSP56. The polynucleotides (PNs) of
 CC the invention encode metastatic marker protein variants. The PNs and
 CC polypeptides can be used as markers for cancer metastasis. The products
 CC can be used for identifying metastatic tissue or metastatic potential of
 CC a tissue, e.g. breast or colon tissue. They can also be used for
 CC screening test compounds for the ability to suppress the metastatic
 CC potential of a tumour. The products can be used for developing products
 CC for the therapy of cancers, particularly breast or colon cancer
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2113; DB 2; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2.2e-198;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ALEPALASPAGAANFLAMVDNLQDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAANFLAMVDNLQDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
QY	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
QY	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
QY	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	302
QY	241	DSGTLLRLRPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	300
Db	303	DSGTLLRLRPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	362
QY	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422

Qy 361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
 |||||
 Db 423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 11

AAY41714

ID AAY41714 standard; protein; 518 AA.
 XX
 AC AAY41714;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human PRO852 protein sequence.
 XX
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9946281-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 08-MAR-1999; 99WO-US005028.
 XX
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.

PR	08-APR-1998;	98US-0081070P.
PR	08-APR-1998;	98US-0081071P.
PR	09-APR-1998;	98US-0081195P.
PR	09-APR-1998;	98US-0081203P.
PR	09-APR-1998;	98US-0081229P.
PR	15-APR-1998;	98US-0081817P.
PR	15-APR-1998;	98US-0081838P.
PR	15-APR-1998;	98US-0081952P.
PR	15-APR-1998;	98US-0081955P.
PR	21-APR-1998;	98US-0082568P.
PR	21-APR-1998;	98US-0082569P.
PR	22-APR-1998;	98US-0082700P.
PR	22-APR-1998;	98US-0082704P.
PR	22-APR-1998;	98US-0082804P.
PR	23-APR-1998;	98US-0082767P.
PR	23-APR-1998;	98US-0082796P.
PR	27-APR-1998;	98US-0083336P.
PR	28-APR-1998;	98US-0083322P.
PR	29-APR-1998;	98US-0083392P.
PR	29-APR-1998;	98US-0083495P.
PR	29-APR-1998;	98US-0083496P.
PR	29-APR-1998;	98US-0083499P.
PR	29-APR-1998;	98US-0083500P.
PR	29-APR-1998;	98US-0083545P.
PR	29-APR-1998;	98US-0083554P.
PR	29-APR-1998;	98US-0083558P.
PR	29-APR-1998;	98US-0083559P.
PR	30-APR-1998;	98US-0083742P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
PR	06-MAY-1998;	98US-0084441P.
PR	07-MAY-1998;	98US-0084598P.
PR	07-MAY-1998;	98US-0084600P.
PR	07-MAY-1998;	98US-0084627P.
PR	07-MAY-1998;	98US-0084637P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	13-MAY-1998;	98US-0085323P.
PR	13-MAY-1998;	98US-0085338P.
PR	13-MAY-1998;	98US-0085339P.
PR	15-MAY-1998;	98US-0085573P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085689P.
PR	15-MAY-1998;	98US-0085697P.
PR	15-MAY-1998;	98US-0085700P.
PR	15-MAY-1998;	98US-0085704P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086392P.
PR	22-MAY-1998;	98US-0086414P.
PR	22-MAY-1998;	98US-0086430P.
PR	22-MAY-1998;	98US-0086486P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087106P.
PR	28-MAY-1998;	98US-0087208P.

PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR N-PSDB; AAZ34056.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS Claim 12; Fig 73; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
CC AAY41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 2113; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.2e-198;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ALEPALASPAGAAANFLAMVDNLQDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
QY	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
QY	121	SEFFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SEFFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS	242
QY	181	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	302
QY	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	362
QY	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422

Qy 361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
 |||||
 Db 423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 12

AA88424

ID AA88424 standard; protein; 518 AA.

XX

AC AA88424;

XX

DT 03-AUG-2000 (first entry)

XX

DE Human aspartyl protease 1 (Asp1) amino acid sequence.

XX

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;
 KW Alzheimer's disease; beta secretase site.

XX

OS Homo sapiens.

XX

PN WO200017369-A2.

XX

PD 30-MAR-2000.

XX

PF 23-SEP-1999; 99WO-US020881.

XX

PR 24-SEP-1998; 98US-0101594P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2000-303209/26.

DR N-PSDB; AAA15661.

XX

PT New enzyme designated human aspartase useful in research into Alzheimer's
 PT Disease is capable of cleaving amyloid protein precursor at the beta
 PT secretase site to produce amyloid beta peptide.

XX

PS Claim 54; Fig 1; 183pp; English.

XX

CC This sequence represents the human aspartyl protease amino acid sequence.
 CC The invention relates to a protease capable of cleaving the beta
 CC secretase site of amyloid precursor protein (APP). The protease contains
 CC a sequence encoding the amino acid sequence DTG and a sequence encoding
 CC DSG or DTG separated by 100-300 amino acids. When mutated the APP gene
 CC causes an autosomal dominant form of Alzheimer's disease. APP localises
 CC to the cell surface membrane and have a single C-terminal transmembrane
 CC domain. Proteolytic processing of APP produces the amyloid beta protein,
 CC which is possibly very important in Alzheimer's disease. The invention
 CC includes a nucleotide sequence encoding the protease, a vector containing
 CC the nucleotide sequence, and a cell line comprising the vector. Methods
 CC for screening for inhibitors of beta secretase activity are also given in
 CC the invention. The human aspartase protein and nucleotide sequences and
 CC the methods for identifying inhibitors of the protease, are useful in the
 CC treatment of and research in to Alzheimer's disease

XX

SQ Sequence 518 AA;

Query Match 100.0%; Score 2113; DB 3; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.2e-198;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
      |||
Db      63 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

QY     61 HSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
      |||
Db    123 HSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

QY    121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
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Db    183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 242

QY    181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 240
      |||
Db    243 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 302

QY    241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL 300
      |||
Db    303 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL 362

QY    301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
      |||
Db    363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

QY    361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
      |||
Db    423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468
```

RESULT 13

AAB44270

ID AAB44270 standard; protein; 518 AA.

XX

AC AAB44270;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human PRO852 (UNQ418) protein sequence SEQ ID NO:196.

XX

KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.

XX

OS Homo sapiens.

XX

PN WO200053756-A2.

XX

PD 14-SEP-2000.

XX

PF 18-FEB-2000; 2000WO-US004341.

XX

PR 08-MAR-1999; 99WO-US005028.

PR 12-MAR-1999; 99US-0123957P.
 PR 29-MAR-1999; 99US-0126773P.
 PR 21-APR-1999; 99US-0130232P.
 PR 28-APR-1999; 99US-0131445P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 DR WPI; 2000-611443/58.
 DR N-PSDB; AAC78500.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods, to
 PT target bioactive molecules to specific cells, and to modulate cellular
 PT activities.
 XX
 PS Claim 12; Fig 73; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
 CC The PRO polynucleotides and polypeptides have cytostatic activity. The
 CC polynucleotides and polypeptides can be used for detecting the presence
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells
 CC and for modulating biological activities of cells, using the polypeptides
 CC for specific targeting. The polypeptide targeting can be used to kill the
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to
 CC AAC78987 represent PCR primers and probes used in the isolation of the
 CC PRO polynucleotide sequences
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2113; DB 3; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2.2e-198;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
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 Db 63 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy	61	HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTIPKGNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTIPKGNTSFLVNIATIFE	182
Qy	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
Qy	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	302
Qy	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	362
Qy	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
Qy	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPII	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPII	468

RESULT 14

AAU07201

ID AAU07201 standard; protein; 518 AA.

XX

AC AAU07201;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human aspartyl protease 1 (Asp-1).

XX

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 KW beta-secretase; Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO200149097-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000797.

XX

PR 09-MAY-2001; 2001WO-IB000797.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502548/55.
 DR N-PSDB; AAS11701.
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity.
 XX
 PS Example 2; Fig 1; 185pp; English.
 XX
 CC The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing an
 CC APP cleavage site recognisable by a mammalian beta-secretase, and further
 CC comprising two lysine residues at the carboxyl terminus of the amino acid
 CC sequence of the mammalian APP or APP fragment. The polypeptides are used
 CC for assaying for modulators of beta-secretase activity; identifying
 CC agents that inhibit the APP processing activity of human Asp2 aspartyl
 CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
 CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
 CC Agents identified by the above methods are useful for treating
 CC Alzheimer's disease; and for identifying modulators of amyloid-beta
 CC (Abeta) peptide production, for use in designing therapeutics for the
 CC treatment or prevention of Alzheimer's disease. Probes and primers
 CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
 CC nucleic acids in in vitro assays and in Northern and Southern blots. The
 CC present sequence represents the amino acid sequence of human Asp-1
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2113; DB 4; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2.2e-198;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEPALASPAGAANFLAMVDNLQDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
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 Db 63 ALEPALASPAGAANFLAMVDNLQDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122
 QY 61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 123 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182
 QY 121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 242
 QY 181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 243 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV 302
 QY 241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 303 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 362

Qy 301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
 |||
 Db 363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422
 Qy 361 QKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
 |||
 Db 423 QKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 15

AAE10628

ID AAE10628 standard; protein; 518 AA.
 XX
 AC AAE10628;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human aspartyl protease 1 (hu-Asp1) protein.
 XX
 KW Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
 KW chromosome 21.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .20
 FT /label= Signal_peptide
 FT Protein 21. .518
 FT /note= "Mature human aspartyl protease 1"
 FT Domain 469. .492
 FT /label= Transmembrane_domain
 XX
 PN GB2357767-A.
 XX
 PD 04-JUL-2001.
 XX
 PF 22-SEP-2000; 2000GB-00023315.
 XX
 PR 23-SEP-1999; 99US-00404133.
 PR 23-SEP-1999; 99US-0155493P.
 PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2001-444208/48.
 DR N-PSDB; AAD17864.
 XX
 PT Polypeptide comprising fragments of human aspartyl protease with amyloid
 PT precursor protein processing activity and alpha-secretase activity, for
 PT identifying modulators useful in treating Alzheimer's disease.
 XX

PS Claim 36; Fig 1; 187pp; English.
 XX
 CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
 CC proteins which lack transmembrane domain or amino terminal domain or
 CC cytoplasmic domain and retains alpha-secretase activity and amyloid
 CC protein precursor (APP) processing activity. The proteins of the
 CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
 CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
 CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
 CC are useful for treating Alzheimer's disease (AD) which causes progressive
 CC dementia with consequent formation of amyloid plaques, neurofibrillary
 CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
 CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
 CC with the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is Asp1 protein from
 CC human. Asp1 gene is localised on chromosome 21
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2113; DB 4; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2.2e-198;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
QY	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATIFE	182
QY	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
QY	181	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	302
QY	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	362
QY	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
QY	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

Search completed: March 4, 2004, 15:35:43
 Job time : 83.0638 secs

OM protein - protein search, using sw model

Run on: March 4, 2004, 15:31:20 ; Search time 26.3468 Seconds
 (without alignments)
 795.548 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
 Perfect score: 2113
 Sequence: 1 ALEPALASPAGAAANFLAMVD.....STEDVASNCVPAQSLSEPIL 406

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2113	100.0	518	3	US-08-999-723-2	Sequence 2, Appli
2	2113	100.0	518	3	US-09-434-427-2	Sequence 2, Appli
3	2113	100.0	518	4	US-09-548-372D-2	Sequence 2, Appli
4	2113	100.0	518	4	US-09-548-367D-2	Sequence 2, Appli
5	2113	100.0	518	4	US-09-551-853D-2	Sequence 2, Appli
6	2113	100.0	518	4	US-09-215-450-19	Sequence 19, Appl
7	1962	92.9	514	3	US-09-717-432-2	Sequence 2, Appli
8	1962	92.9	514	4	US-09-912-484-2	Sequence 2, Appli
9	1133	53.6	501	4	US-09-713-158-2	Sequence 2, Appli
10	1133	53.6	501	4	US-09-548-372D-8	Sequence 8, Appli
11	1133	53.6	501	4	US-09-548-367D-8	Sequence 8, Appli

12	1133	53.6	501	4	US-09-551-853D-8	Sequence 8, Appli
13	1133	53.6	501	4	US-09-724-566A-65	Sequence 65, Appl
14	1132	53.6	407	4	US-09-724-566A-58	Sequence 58, Appl
15	1132	53.6	431	4	US-09-724-566A-74	Sequence 74, Appl
16	1132	53.6	452	4	US-09-724-566A-59	Sequence 59, Appl
17	1132	53.6	453	4	US-09-548-372D-30	Sequence 30, Appl
18	1132	53.6	453	4	US-09-548-367D-30	Sequence 30, Appl
19	1132	53.6	453	4	US-09-551-853D-30	Sequence 30, Appl
20	1132	53.6	456	4	US-09-724-566A-43	Sequence 43, Appl
21	1132	53.6	459	4	US-09-548-372D-32	Sequence 32, Appl
22	1132	53.6	459	4	US-09-548-367D-32	Sequence 32, Appl
23	1132	53.6	459	4	US-09-551-853D-32	Sequence 32, Appl
24	1132	53.6	480	4	US-09-724-566A-66	Sequence 66, Appl
25	1132	53.6	488	4	US-09-604-608-2	Sequence 2, Appli
26	1132	53.6	501	4	US-09-548-372D-4	Sequence 4, Appli
27	1132	53.6	501	4	US-09-548-367D-4	Sequence 4, Appli
28	1132	53.6	501	4	US-09-551-853D-4	Sequence 4, Appli
29	1132	53.6	501	4	US-09-724-566A-2	Sequence 2, Appli
30	1132	53.6	503	4	US-09-604-608-3	Sequence 3, Appli
31	1128	53.4	395	4	US-09-724-566A-68	Sequence 68, Appl
32	1128	53.4	444	4	US-09-724-566A-67	Sequence 67, Appl
33	1127	53.3	433	4	US-09-548-372D-26	Sequence 26, Appl
34	1127	53.3	433	4	US-09-548-367D-26	Sequence 26, Appl
35	1127	53.3	433	4	US-09-551-853D-26	Sequence 26, Appl
36	1127	53.3	446	4	US-09-548-372D-22	Sequence 22, Appl
37	1127	53.3	446	4	US-09-548-367D-22	Sequence 22, Appl
38	1127	53.3	446	4	US-09-551-853D-22	Sequence 22, Appl
39	1127	53.3	459	4	US-09-548-372D-24	Sequence 24, Appl
40	1127	53.3	459	4	US-09-548-367D-24	Sequence 24, Appl
41	1127	53.3	459	4	US-09-551-853D-24	Sequence 24, Appl
42	1126	53.3	501	4	US-09-009-191-2	Sequence 2, Appli
43	1123	53.1	425	4	US-09-548-372D-28	Sequence 28, Appl
44	1123	53.1	425	4	US-09-548-367D-28	Sequence 28, Appl
45	1123	53.1	425	4	US-09-551-853D-28	Sequence 28, Appl

ALIGNMENTS

```

RESULT 1
US-08-999-723-2
; Sequence 2, Application US/08999723A
; Patent No. 6025180
; GENERAL INFORMATION:
; APPLICANT: Powell, David J.
; APPLICANT: Southan, Christopher
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Evans, Joanne R.
; TITLE OF INVENTION: ASPl
; FILE REFERENCE: GH70262
; CURRENT APPLICATION NUMBER: US/08/999,723A
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-08-999-723-2

Query Match 100.0%; Score 2113; DB 3; Length 518;
Best Local Similarity 100.0%; Pred. No. 7e-210;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy      61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

Qy     121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANI PNVFMSQMCGAGLPVAGS 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANI PNVFMSQMCGAGLPVAGS 242

Qy     181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 302

Qy     241 DSGTTLRLRPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     303 DSGTTLRLRPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 362

Qy     301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

Qy     361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468
```

RESULT 2

US-09-434-427-2

; Sequence 2, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518

; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-434-427-2

Query Match 100.0%; Score 2113; DB 3; Length 518;
Best Local Similarity 100.0%; Pred. No. 7e-210;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy     61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

Qy    121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 242

Qy    181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 302

Qy    241 DSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 DSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL 362

Qy    301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

Qy    361 QKRVGFAASPCA EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 QKRVGFAASPCA EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468
```

RESULT 3

US-09-548-372D-2

; Sequence 2, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-2

Query Match 100.0%; Score 2113; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 7e-210;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
Qy	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGENTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGENTSFLVNIATIFE	182
Qy	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS	242
Qy	181	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	302
Qy	241	DSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	300
Db	303	DSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	362
Qy	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
Qy	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 4

US-09-548-367D-2

; Sequence 2, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-2

Query Match 100.0%; Score 2113; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 7e-210;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy      61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGVGEDLVTIPKGFNTSFLVNIATIFE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGVGEDLVTIPKGFNTSFLVNIATIFE 182

Qy     121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 242

Qy     181 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV 302

Qy     241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     303 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 362

Qy     301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

Qy     361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468
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RESULT 5

US-09-551-853D-2

; Sequence 2, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 518
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-551-853D-2

Query Match 100.0%; Score 2113; DB 4; Length 518;
 Best Local Similarity 100.0%; Pred. No. 7e-210;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
Qy	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATIFE	182
Qy	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
Qy	181	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	302
Qy	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	362
Qy	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
Qy	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 6

US-09-215-450-19

; Sequence 19, Application US/09215450

; Patent No. 6635748

; GENERAL INFORMATION:

; APPLICANT: Giese, Klaus

; APPLICANT: Xin, Hong

; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES

; FILE REFERENCE: 1451.100 / 210030.447
; CURRENT APPLICATION NUMBER: US/09/215,450
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 518
; TYPE: PRT
; ORGANISM: human
US-09-215-450-19

Query Match 100.0%; Score 2113; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 7e-210;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy      61 HSYIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 HSYIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

Qy     121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS 242

Qy     181 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 302

Qy     241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     303 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL 362

Qy     301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

Qy     361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI L 406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI L 468
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RESULT 7

US-09-717-432-2

; Sequence 2, Application US/09717432
; Patent No. 6291223
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; APPLICANT: LI, XIAOTONG
; APPLICANT: CHRISTIE, GARY
; APPLICANT: POWELL, DAVID J.
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mASP1)
; FILE REFERENCE: GP-70663
; CURRENT APPLICATION NUMBER: US/09/717,432
; CURRENT FILING DATE: 2000-11-21

; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-717-432-2

Query Match 92.9%; Score 1962; DB 3; Length 514;
Best Local Similarity 91.6%; Pred. No. 3e-194;
Matches 372; Conservative 15; Mismatches 15; Indels 4; Gaps 1;

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Qy      1 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
      |||| | : |||||||||||||||||||||||||||||||||||||||
Db      63 ALEPVRAT----ANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKVQILVDTGSSNFAVAGAP 118

Qy      61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
      ||||||||:| |||| |||||||||||||||||||||||||||||:|||||||
Db     119 HSYIDTYFDSESSSTYHSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNSSFLVNIATIFE 178

Qy     121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS 180
      |||||||||||||||||| |||||||||||||||| || ||:|||||||||
Db     179 SENFFLPGIKWNGILGLAYAALAKPSSSLETFDLSLVAQAKIPDIFSMQMCAGLPVAGS 238

Qy     181 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 240
      |||||||||||||||||| |||||||||||||||| ||:|||||||||
Db     239 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 298

Qy     241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL 300
      |||||||||||||||||| ||||||||||||||||:|||||||||:|||||||
Db     299 DSGTTLLRLPQKVFDVAVVEAVARTSLIPEFSDGFWTGAQLACWTNSETPWAYFPKISIYL 358

Qy     301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
      ||||:|||||||||||||||| |||||||| ||||||||||||||||:||||
Db     359 RDENASRSFRITILPQLYIQPMMGAGFNYECYRFGISSSTNALVIGATVMEGFYVIFDRA 418

Qy     361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
      |:|||| ||||| | ||||||||||||:|||||||:|:||||
Db     419 QRRVGFAVSPCAIEIEGTTVSEISGPFSTEDIASNCVPAQALNEPIL 464
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RESULT 8

US-09-912-484-2

; Sequence 2, Application US/09912484
; Patent No. 6358725
; GENERAL INFORMATION:
; APPLICANT: Christie, Gary
; APPLICANT: Li, Xiaotong
; APPLICANT: Powell, David J.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mASP1)
; FILE REFERENCE: GP-70663-D1
; CURRENT APPLICATION NUMBER: US/09/912,484
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/166,974

; PRIOR APPLICATION NUMBER: 60/165,800
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-713-158-2

Query Match 53.6%; Score 1133; DB 4; Length 501;
Best Local Similarity 53.7%; Pred. No. 2e-108;
Matches 208; Conservative 65; Mismatches 110; Indels 4; Gaps 2;

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Qy      9  PAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYF 68
          |      :|: |||||:| ||:||||:| | :|:| | | ||||| ||||| | | :|: |
Db      54  PGRRGSEFVEMVDNLRGKSGQGYVEMTVGSPQTLNILVDTGSSNFAVGAAPHPFLHRY 113

Qy     69  DTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFFLPG 128
          : ||||| | | |||| | | :| |||:| | | | : || | ||: ||: |
Db    114  QRQLSSTYRDLRKGVPYPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFING 173

Qy    129  IKWNGILGLAYATLAKPSSSLETFFDLSVTQANIPNVFSMQMCGAGLPV---AGSGTNGG 185
          | ||||| | | :|:| || | |||| | | :|||:| |:| | | : ||
Db    174  SNWEGILGLAYAEIARPDDSLEPFDSLQKQTHIPNIFSLQLCGAGFPLNQTEALASVGG 233

Qy    186  SLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTT 245
          |:::| | | | | :| | | | | | | | | | | | | | | | | | | | | |
Db    234  SMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTT 293

Qy    246  LLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENS 305
          ||||:| | | | | | | | | | | | | | | | | | | | | | |
Db    294  NLRLPKKVFEAAVKSIAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLYLMGEVT 353

Qy    306  SRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV 364
          :| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    354  NQSFRTILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRI 413

Qy    365  GFAASPCAIEIAGAAVSEISGPFSTEDV 391
          ||| | | | : : ||| | | :
Db    414  GFAVSACHVHDEFRTAAVEGPFVTADM 440
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RESULT 10

US-09-548-372D-8

; Sequence 8, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

```

; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 501
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-548-372D-8

```

```

RESULT 11
US-09-548-367D-8
; Sequence 8, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H

```



```

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-551-853D-8

```

```

Query Match          53.6%; Score 1133; DB 4; Length 501;
Best Local Similarity 53.7%; Pred. No. 2e-108;
Matches 208; Conservative 65; Mismatches 110; Indels 4; Gaps 2;

```

```

Qy      9 PAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYF 68
      | :|: |||||:| ||:||||:| |:| || | ||||| ||||| || :| :| :|
Db      54 PGRRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILVDTGSSNFAVGAAPHPFLHRY 113

Qy      69 DTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITPKGENTSFLVNIATIFESENFPLPG 128
      : ||||| | | |||| | | :| |||:| | | : | | | | ||: ||: |
Db      114 QRQLSSTYRDLRKG VYVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFING 173

Qy      129 IKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV---AGSGTNGG 185
      | ||||| ||| :|:| ||| ||||| | :|||:| |:| ||| | : | |
Db      174 SNWEGILGLAYAEIARPDDSLEPFFDSL VKQTHIPNIFSLQLCGAGFPLNQTEALASVGG 233

Qy      186 SLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTT 245
      |:::| ||: ||| | :||| |: |||:| |:|:| | | :||:| ||:| |||||
Db      234 SMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTT 293

Qy      246 LLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISYLRDENS 305
      |||:| ||:| |::: || :| |||| | || || |||: || ||:| | :|
Db      294 NLRLPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVT 353

Qy      306 SRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV 364
      ::||| ||||| |::| : : ||:| :| | : || :||| |:|||:| |:|
Db      354 NQSFRTILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRI 413

Qy      365 GFAASPCAIEIAGAAVSEISGPFSTEDV 391
      ||| | | : : ||| | |:|
Db      414 GFAVSACHVHDEFRTAAVEGPFVVTADM 440

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RESULT 13
 US-09-724-566A-65

```
; Sequence 65, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-566A-65
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Qy 306 SRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV 364
 ::||||||| |::| : :||:| :| |: |:| :|||||:||||:|:
 Db 354 NQSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRI 413

Qy 365 GFAASPCAIEIAGAAVSEISGPFSTEDV 391
 ||| | | : : ||| | |:
 Db 414 GFAVSACHVHDEFRTAAVEGPFVTADM 440

RESULT 14

US-09-724-566A-58

; Sequence 58, Application US/09724566A
 ; Patent No. 6627739
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Basi, Gurigbal
 ; APPLICANT: Doane, Minh Tam
 ; APPLICANT: Frigon, No. 6627739mand
 ; APPLICANT: John, Varghese
 ; APPLICANT: Power, Michael
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Tatsuno, Gwen
 ; APPLICANT: Tung, Jay
 ; APPLICANT: Wang, Shuwen
 ; APPLICANT: McConlogue, Lisa
 ; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
 ; TITLE OF INVENTION: Methods
 ; FILE REFERENCE: 228-US-NEWC2
 ; CURRENT APPLICATION NUMBER: US/09/724,566A
 ; CURRENT FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 09/501,708
 ; PRIOR FILING DATE: 2000-02-10
 ; PRIOR APPLICATION NUMBER: 60/119,571
 ; PRIOR FILING DATE: 1999-02-10
 ; PRIOR APPLICATION NUMBER: 60/139,172
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 58
 ; LENGTH: 407
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-724-566A-58

Query Match 53.6%; Score 1132; DB 4; Length 407;
 Best Local Similarity 54.0%; Pred. No. 1.8e-108;
 Matches 209; Conservative 65; Mismatches 109; Indels 4; Gaps 2;

Qy 9 PAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYF 68
 | :|: |||||:| ||:||||:| :|:| | | ||||| | | || :|:
 Db 9 PGRRGSFVEMVDNLRGKSGQGYVEMTVGSPQTLNILVDTGSSNFAVGAAPHPFLHRY 68

Qy 69 DTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFPLPG 128
 : ||||| | | |||| | | :| |||:| | | : ||| | ||: ||: |
 Db 69 QRQLSSTYRDLRKGVPYPTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFING 128

Qy 129 IKWNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPVAGS---GTNGG 185

Db	129	SNWEGILGLAYAEIARPDDSLPEFFDSLQTHVPNLFSLQLCGAGFPLNQSEVLASVGG	188
Qy	186	SLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTT	245
Db	189	SMIIGGIDHSLYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTT	248
Qy	246	LLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENS	305
Db	249	NRLPKKVFEAAVKSIAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVT	308
Qy	306	SRSFRITILPQLYIQPMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV	364
Db	309	NQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRI	368
Qy	365	GFAASPCAIEIAGAAVSEISGPFSTEDV	391
Db	369	GFAVSACHVHDEFRTAAVEGPFVTLDM	395

RESULT 15

US-09-724-566A-74

; Sequence 74, Application US/09724566A

; Patent No. 6627739

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Guriqbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, No. 6627739mand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto

; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay

; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and

; TITLE OF INVENTION: Methods

; FILE REFERENCE: 228-US-NEWC2

; CURRENT APPLICATION NUMBER: US/09/724,566A

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/501,708

; PRIOR FILING DATE: 2000-02-10

; PRIOR APPLICATION NUMBER: 60/119,571

; PRIOR FILING DATE: 1999-02-10

; PRIOR APPLICATION NUMBER: 60/139,172

; PRIOR FILING DATE: 1999-06-15

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 74

; LENGTH: 431

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-566A-74

Query Match	53.6%;	Score 1132;	DB 4;	Length 431;
Best Local Similarity	54.0%;	Pred. No. 2e-108;		

Matches 209; Conservative 65; Mismatches 109; Indels 4; Gaps 2;

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Qy      9 PAGAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYF 68
      |   :|: |||||:| ||:||||:| | :|:| | | ||||| ||||| | | :|: | :
Db     33 PGRRGSFVEMVDNLRGKSGQGYVEMTVGSPQTLNILVDTGSSNFAVGAAPHPFLHRY 92

Qy     69 DTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENFFLPG 128
      : ||||| | | |||| | | :| |||:| | | | : ||| | ||: ||: |
Db     93 QRQLSSTYRDLRKGVPYPTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFING 152

Qy    129 IKWNGILGLAYATLAKPSSSLETFEFDLVTQANIPNVFSMQMCGAGLPVAGS---GTNGG 185
      | ||||| ||| :|:| ||| ||||| | :||:| |:| ||| | : | |
Db    153 SNWEGILGLAYAEIARPDDSLEPFEDSLVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGG 212

Qy    186 SLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTT 245
      |:::| |:| ||| | :||| |: |||:| |:::| | | :||:| ||:| |||||
Db    213 SMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTT 272

Qy    246 LLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENS 305
      |||:| |:| |::: | | :| ||| | || | | |||: | | ||:| | | :
Db    273 NLRLPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVT 332

Qy    306 SRSFRITILPQLYIQPMMGAGLNY-ECYREGISPSTNALVIGATVMEGFYVIFDRAQKRV 364
      ::||| ||||| |::| : : ||:| || | : |::| :||| |::|:| |:|
Db    333 NQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRI 392

Qy    365 GFAASPCAIEIAGAAVSEISGPFSTEDV 391
      ||| | | : : ||| | | :
Db    393 GFAVSACHVHDEFRTAAVEGPFVTLDM 419
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Search completed: March 4, 2004, 15:42:14
Job time : 27.3468 secs

OM protein - protein search, using sw model

Run on: March 4, 2004, 15:30:05 ; Search time 22.0277 Seconds
 (without alignments)
 1772.942 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
 Perfect score: 2113
 Sequence: 1 ALEPALASPAGAANFLAMVD.....STEDVASNCVPAQSLSEPIL 406

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1132	53.6	501	2	A59090	aspartic proteinas
2	359.5	17.0	377	1	PEMQCJ	gastricsin (EC 3.4
3	355	16.8	389	2	JE0371	pepsin C (EC 3.4.2
4	351.5	16.6	388	2	JC7246	pepsinogen C - com
5	350.5	16.6	388	2	A29937	gastricsin (EC 3.4
6	346.5	16.4	383	2	JC7573	pepsinogen C - Afr
7	339.5	16.1	384	2	A39314	gastricsin (EC 3.4
8	324.5	15.4	394	2	B43356	gastricsin (EC 3.4
9	318	15.0	385	2	JC7575	pepsinogen A - bul
10	313	14.8	392	1	A24608	gastricsin (EC 3.4
11	306.5	14.5	383	2	A41443	pepsin (EC 3.4.23.
12	306.5	14.5	410	1	KHMSD	cathepsin D (EC 3.
13	305	14.4	407	1	KHRTD	cathepsin D (EC 3.

14	304	14.4	402	1	REMSK	renin (EC 3.4.23.1
15	302	14.3	384	2	JC7574	pepsinogen A - Afr
16	302	14.3	405	2	A25379	saccharopepsin (EC
17	301.5	14.3	398	2	S66465	cathepsin E (EC 3.
18	298.5	14.1	412	1	KHHUD	cathepsin D (EC 3.
19	297	14.1	387	2	C38302	pepsin (EC 3.4.23.
20	297	14.1	388	1	PEHU	pepsin A (EC 3.4.2
21	296	14.0	388	2	A30142	pepsin A (EC 3.4.2
22	296	14.0	388	2	B30142	pepsin A (EC 3.4.2
23	296	14.0	398	2	I51185	cathepsin D (EC 3.
24	296	14.0	401	1	REMSS	renin (EC 3.4.23.1
25	294	13.9	388	1	S19684	pepsin A (EC 3.4.2
26	294	13.9	400	2	I47099	renin (EC 3.4.23.1
27	293	13.9	387	2	D38302	pepsin (EC 3.4.23.
28	291	13.8	388	1	S19682	pepsin A (EC 3.4.2
29	291	13.8	406	1	REHUK	renin (EC 3.4.23.1
30	290.5	13.7	396	2	S36865	cathepsin E (EC 3.
31	290	13.7	402	1	RERTK	renin (EC 3.4.23.1
32	289	13.7	387	2	E38302	pepsin (EC 3.4.23.
33	288	13.6	387	2	B38302	pepsin (EC 3.4.23.
34	288	13.6	388	1	PEMQAJ	pepsin A (EC 3.4.2
35	287.5	13.6	509	2	S66516	oryzasin (EC 3.4.2
36	287.5	13.6	632	2	T45858	hypothetical prote
37	287	13.6	391	2	A43356	cathepsin E (EC 3.
38	287	13.6	396	2	A34401	cathepsin E (EC 3.
39	286	13.5	382	1	PECH	pepsin A (EC 3.4.2
40	286	13.5	388	1	PEMQAR	pepsin A (EC 3.4.2
41	285.5	13.5	387	2	JC7245	pepsinogen A - com
42	285	13.5	506	2	T07915	probable aspartic
43	284.5	13.5	386	1	PEPG	pepsin A (EC 3.4.2
44	284.5	13.5	508	2	D85056	probable aspartic
45	282.5	13.4	381	1	CMSHB	chymosin (EC 3.4.2

ALIGNMENTS

RESULT 1

A59090

aspartic proteinase (EC 3.4.23.-) BACE precursor - human

N;Alternate names: beta-secretase; beta-site APP cleaving enzyme

C;Species: Homo sapiens (man)

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-May-2000

C;Accession: A59090

R;Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Denis, P.; Teplow, D.B.; Ross, S.; Amarante, P.; Loeloff, R.; Luo, Y.; Fisher, S.; Fuller, J.; Edenson, S.; Lile, J.; Jarosinski, M.A.; Biere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Rogers, G.; Citron, M.
Science 286, 735-741, 1999

A;Title: beta-Secretase cleavage of Alzheimer's amyloid precursor protein by the transmembrane aspartic protease BACE.

A;Reference number: A59090; MUID:20002972; PMID:10531052

A;Note: submitted to GenBank, September 1999

A;Accession: A59090

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-501 <VAS>

A;Title: Development-dependent expression of isozymogens of monkey pepsinogens and structural differences between them.
A;Reference number: S19681; MUID:92037645; PMID:1935977
A;Accession: S19683
A;Molecule type: mRNA
A;Residues: 1-377 <KAG>
A;Cross-references: EMBL:X59754; NID:g38072; PIDN:CAA42426.1; PID:g38073
R;Kageyama, T.; Takahashi, K.
J. Biol. Chem. 261, 4406-4419, 1986
A;Title: The complete amino acid sequence of monkey progastricsin.
A;Reference number: A00986; MUID:86168133; PMID:3514597
A;Accession: A00986
A;Molecule type: protein
A;Residues: 6-330,'V',332-349,'VY',350-377 <KA2>
R;Kageyama, T.; Takahashi, K.
J. Biochem. 97, 1235-1246, 1985
A;Title: Monkey pepsinogens and pepsins. VII. Analysis of the activation process and determination of the NH2-terminal 60-residue sequence of Japanese monkey progastricsin, and molecular evolution of pepsinogens.
A;Reference number: A22402; MUID:85289106; PMID:3928607
A;Accession: A22402
A;Molecule type: protein
A;Residues: 6-65 <KA3>
C;Comment: This enzyme has more restricted specificity than pepsin A.
C;Comment: The enzyme is activated in a two-step process that gives rise to two end products. The shorter, Ser-gastricsin, is the major product.
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion; stomach
F;1-5/Domain: signal sequence (fragment) #status predicted <SIG>
F;6-377/Product: progastricsin #status experimental <ZYM>
F;6-45/Domain: activation peptide #status experimental <APT>
F;46-377/Product: Gly-gastricsin #status experimental <MIN>
F;49-377/Product: Ser-gastricsin #status experimental <MAT>
F;31-32/Cleavage site: Phe-Leu (pepsin) #status experimental
F;45-46/Cleavage site: Phe-Gly (pepsin) #status experimental
F;48-49/Cleavage site: Leu-Ser (pepsin) #status experimental
F;80,265/Active site: Asp #status predicted
F;93-98,256-260,299-332/Disulfide bonds: #status experimental

Query Match 17.0%; Score 359.5; DB 1; Length 377;
Best Local Similarity 30.1%; Pred. No. 7.5e-21;
Matches 112; Conservative 60; Mismatches 111; Indels 89; Gaps 17;

QY	30	YYLEMLIGTPPQKLQILVDTGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGF	81
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Db	62	YFGEISIGTPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHS----RFNPSESSTYSTNGQ	117
QY	82	DVTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATIFESENFFLPG-----IKWNGILG	136
		::: : :	
Db	118	TFSLQYGSGLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMG	170
QY	137	LAYATLAKPSSSLETFFDSLVTQANIPN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPS	195
		: :: : : : : : : :: :: ::	
Db	171	LAYPTLSVDGAT--TAMQGMVQEGALTSPIFSVYLSAQ-----QGSSGGAVVFGGVDSS	222
QY	196	LYKGGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVFD	255

```

      || | |:: |: :| |::| | : |::| : |::| |::| |::|
Db      223 LYTGQIYWAPVTQELYWQIGIEEFLIGGQASGW-CSE--GCQAIVDTGTSLLTVPQQYMS 279
Qy      256 AVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYF-----PKISIIYLRDENS 305
      |:::| |::| | : | |:: :
Db      280 ALLQA-----TGAQ-----EDEYGQFLVNCNSIQNLPTLTFII----- 312
Qy      306 SRSFRITILPQLYIQPMMGAGLNYECY-RFGISP-----STNALVIGATVMEGFYVIF 357
      : | || | | | : | | : | : :
Db      313 -NGVEFPLPPSSYI-----LNNNGYCTVGVEPTYLSAQNSQPLWILGDVFLRSYYSVY 364
Qy      358 DRAQKRVGFSAAS 369
      | : |::| :
Db      365 DLSNNRVGFATA 376

```

RESULT 3

JE0371

pepsin C (EC 3.4.23.-) precursor - chicken

N;Alternate names: pepsinogen C

C;Species: Gallus gallus (chicken)

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000

C;Accession: JE0371

R;Sakamoto, N.; Saiga, H.; Yasugi, S.

Biochem. Biophys. Res. Commun. 250, 420-424, 1998

A;Title: Analysis of temporal expression pattern and cis-regulatory sequences of chicken pepsinogen A and C.

A;Reference number: JE0370; MUID:98440813; PMID:9753645

A;Accession: JE0371

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-389 <SAK>

C;Superfamily: pepsin

C;Keywords: aspartic proteinase; hydrolase

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Query Match          16.8%;  Score 355;  DB 2;  Length 389;
Best Local Similarity 28.7%;  Pred. No. 1.8e-20;
Matches 114;  Conservative 58;  Mismatches 121;  Indels 104;  Gaps 16;

```

```

Qy      13 ANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGT-----PHSYI 64
      :|| : | : || |: ||||| :| ||||| | | |
Db      56 SNEATAYEPLANNMDMSYYGEISIGTPPQNFLVLFDTGSSNLWVPSTLCQSQAACANHN-- 113
Qy      65 DTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTPKGFN-----TS 110
      || ||:: :: ::| || || | | || :| : ||
Db      114 --EFDPNESSTFSTQDEFFSLQYGSGLTGIFGFDVTI-QGISITNQEFGLSETEPGTS 170
Qy      111 FLVNIATIFESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPN--VFSM 168
      || : :||::|:: :: | : | : | : : ||
Db      171 FLYS-----PFDGILGLAFPSI---SAGGATTVMQKMLQENLLDFPVFSF 212
Qy      169 QMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNL 228
      : | | : || || ||::|::| | | :||: : |::| | :|||
Db      213 YLSGQ-----EGSQGGELVFGGVDPNLYTGQITWTPVTQTTYWQIGIEDFAVGGQSSGW 266
Qy      229 DCREYNADKAIVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSET 288
      | : : ||::|::| :| :|| ::: : : | :| :| :| |

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Db      267 -CSQ--GCQGIVDTGTSLLTVPNQVFTELMQYIG-----AQADD---SGQYVASCSNIE- 314
Qy      289 PWSYFPKI-----SIYLRDENS---SRSFRITILPQLYIQPMMGAGLNYECY 332
        | | |               | | :   ||   :       | | |   || :
Db      315 ---YMPTITFVISGTSFPLPPSAYMLQSNSDYCTVGIESTYLPSQTGQPLW----- 362
Qy      333 RFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAAS 369
        : : |   :   : | | : |   : | | | :
Db      363 -----ILGDVFLRVYYSIYDMGNNQVGFATA 388

```

RESULT 4

JC7246

pepsinogen C - common marmoset

C;Species: Callithrix jacchus (common marmoset)

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text change 21-Jul-2000

C;Accession: JC7246

R; Kageyama, T.

J. Biochem. 127, 761-770, 2000

A;Title: New world monkey pepsinogens A and C, and prochymosins. Purification, characterization of enzymatic properties, cDNA cloning, and molecular evolution.

A;Reference number: JC7245

A;Accession: JC7246

A;Molecule type: mRNA

A;Residues: 1-388 <KAG>

A;Cross-references: DDBJ:AB038385

A;Experimental source: strain NW791

C;Comment: This protein, a zymogen of pepsins, is the major proteolytic enzyme in vertebrate gastric juices. It plays roles in gastric digestion, and is a useful molecular marker for clarifying the evolution of mammalian orders and families.

C;Superfamily: pepsin

C;Keywords: gastric juice; zymogen

Query Match 16.6%; Score 351.5; DB 2; Length 388;
Best Local Similarity 30.1%; Pred. No. 3.4e-20;
Matches 112; Conservative 56; Mismatches 115; Indels 89; Gaps 17;

QY	30	YYLEMLIGTPPQKLQILVDTGSSNFAV-----AGTPHSYIDTYFDTERSSSTYRSKGF	81
		: : : :	
Db	73	YFGEISIGTPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHS----RFNPSASSTYSSNGQ	128
QY	82	DVTVKYTQGSWTGFGVGEDLVTIPKGFNTSFLVNIATIFESENFFLPG-----IKWNGILG	136
		: : : : : : : :	
Db	129	TFSLQYGSGLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMG	181
QY	137	LAYATLAKPSSSLETFFDSLVTQANIPN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPS	195
		: : : : : : : : : : : : :	
Db	182	LAYPALSMGGAT--TAMQGMLQEGALTSPVFSFYLSNQ-----QGSSGGAVIFGGVDSS	233
QY	196	LYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTLLRLPQKVFD	255
		: : : : : : : : :	
Db	234	LYTGQIYWAPVTQELYWQIGIEEFLIGGQASGW-CSE--GCQAIVDTGTSLLTVPQQYMS	290
QY	256	AVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYF-----PKISIIYLRDENS	305
		: : : : : : :	
Db	291	AFLEA-----TGAQ-----EDEYGQFLVNCDSIQNLPTLTFTII-----	323

Qy 306 SRSEFRITILPQLYIQPMMGAGLNYECY-RFGISP-----STNALVIGATVMEGFYVIF 357
 : | || | : | : | : | : | : | : |
 Db 324 -NGVEFPLPPSSYI-----LSNNGYCTVGVEPTYLSSQNSQPLWILGDVFLRSYYSVF 375
 Qy 358 DRAQKRVGFAAS 369
 | |||| :
 Db 376 DLGNNRVGFATA 387

RESULT 5

A29937

gastricsin (EC 3.4.23.3) precursor - human

N;Alternate names: pepsin C; pepsinogen C

C;Species: Homo sapiens (man)

C;Date: 17-Oct-1988 #sequence_revision 17-Oct-1988 #text_change 31-Mar-2000

C;Accession: A29937; A31811; PX0028; I54213; A91125; A23458

R;Hayano, T.; Sogawa, K.; Ichihara, Y.; Fujii-Kuriyama, Y.; Takahashi, K.
 J. Biol. Chem. 263, 1382-1385, 1988

A;Title: Primary structure of human pepsinogen C gene.

A;Reference number: A29937; MUID:88087276; PMID:3335549

A;Accession: A29937

A;Molecule type: DNA

A;Residues: 1-388 <HAY>

R;Taggart, R.T.; Cass, L.G.; Mohandas, T.K.; Derby, P.; Barr, P.J.; Pals, G.;
 Bell, G.I.

J. Biol. Chem. 264, 375-379, 1989

A;Title: Human pepsinogen C (progastricsin). Isolation of cDNA clones,
 localization to chromosome 6, and sequence homology with pepsinogen A.

A;Reference number: A31811; MUID:89079679; PMID:2909526

A;Accession: A31811

A;Molecule type: mRNA

A;Residues: 1-388 <TAG>

A;Cross-references: GB:J04443; NID:g551175; PIDN:AAA60074.1; PID:g551176

R;Athauda, S.B.P.; Tanji, M.; Kageyama, T.; Takahashi, K.

J. Biochem. 106, 920-927, 1989

A;Title: A comparative study on the NH2-terminal amino acid sequences and some
 other properties of six isozymic forms of human pepsinogens and pepsins.

A;Reference number: PX0023; MUID:90130402; PMID:2515193

A;Accession: PX0028

A;Molecule type: protein

A;Residues: 17-101 <ATH>

R;Pals, G.; Azuma, T.; Mohandas, T.K.; Bell, G.I.; Bacon, J.; Samloff, I.M.;
 Walz, D.A.; Barr, P.J.; Taggart, R.T.

Genomics 4, 137-148, 1989

A;Title: Human pepsinogen C (progastricsin) polymorphism: evidence for a single
 locus located at 6p21.1-pter.

A;Reference number: I54213; MUID:89290840; PMID:2567697

A;Accession: I54213

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-388 <RES>

A;Cross-references: GB:M23077; NID:g189830; PIDN:AAA60063.1; PID:g387015;
 GB:J03063

A;Note: parts of this sequence, including the amino end and carboxyl ends of the
 mature protein, were determined by protein sequencing

R;Foltmann, B.; Jensen, A.L.

Eur. J. Biochem. 128, 63-70, 1982

A;Title: Human progastricsin. Analysis of intermediates during activation into gastricsin and determination of the amino acid sequence of the propart.

A;Reference number: A91125; MUID:83079318; PMID:6816595

A;Accession: A91125

A;Molecule type: protein

A;Residues: 17-39,'ED',42-51,'S',53-64 <FOL>

A;Note: pro-form; 29-Leu was also found

A;Note: activation at pH 2 is proposed to involve conformation change, cleavage after Phe-42, and cleavage after Leu-59

C;Genetics:

A;Gene: GDB:PGC

A;Cross-references: GDB:119485; OMIM:169740

A;Map position: 6p21.3-6p21.1

A;Introns: 20/2; 70/3; 110/1; 149/3; 216/2; 256/2; 305/3; 338/3

C;Superfamily: pepsin

C;Keywords: aspartic proteinase; hydrolase; protein digestion; stomach; zymogen

F;1-16/Domain: signal sequence #status predicted <SIG>

F;17-59/Domain: propeptide #status experimental <PRO>

F;60-388/Product: gastricsin #status experimental <MAT>

Query Match 16.6%; Score 350.5; DB 2; Length 388;

Best Local Similarity 30.1%; Pred. No. 4e-20;

Matches 112; Conservative 59; Mismatches 112; Indels 89; Gaps 18;

```
QY      30 YYLEMLIGTPPQKLQILVDTGSSNEFAV-----AGTPHSYIDTYFDTERSSTYRSKGF 81
      |: |: ||||| :| ||||| | | | | | | | | | | | | | | | | | | |
Db      73 YFGEISIGTPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHS----RFNPSESSTYSTNGQ 128

QY      82 DVTVKYTQGSWTGFGEDLVTPKGFNTSFLVNIATIFESENFPLPG-----IKWNGILG 136
      ::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     129 TFSLQYGSGLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMG 181

QY     137 LAYATLAKPSSSLETFFDSLVTQANIPN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPS 195
      ||| |: :: | : : : | | | : | : | | | : | : | | | : |
Db     182 LAYPALSVDEAT--TAMQGMVQEGALTSPVFSVYLSNQ-----QGSSGGAVVFGGVDSS 233

QY     196 LYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVFD 255
      || | |:: |: :| |::| | : ||||: | | : ||||: ||: || : ||:
Db     234 LYTGQIYWAPVTQELYWQIGIEEFLIGGQASGW-CSE--GCQAIVDTGTSLTVPQQYMS 290

QY     256 AVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYF-----PKISYLRDENS 305
      |:::| | | | | | | | | | | | | | | | | | | | | | | | | |
Db     291 ALLQA-----TGAQ-----EDEYQGFLVNCNSIQNLPSLTFII----- 323

QY     306 SRSFRITILPQLYIQPMMGAGLNYECY-RFGISP----STNA---LVIGATVMEGFYVIF 357
      : | || | : | | : | | | : | | : | | : | : | : | : |
Db     324 -NGVEFPLPPSSYI-----LSNNGYCTVGVEPTYLSSQNGQPLWILGDVFLRSYYSVY 375

QY     358 DRAQKRVGFAAS 369
      | | | | | :
Db     376 DLGNRRVGFATA 387
```

RESULT 6

JC7573

pepsinogen C - African clawed frog

N;Alternate names: progastricsin
 C;Species: *Xenopus laevis* (African clawed frog)
 C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C;Accession: JC7573; PC7118
 R;Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.
 J. Biochem. 129, 147-153, 2001
 A;Title: Amphibian pepsinogens: Purification and characterization of *Xenopus* pepsinogens, and molecular cloning of *Xenopus* and bullfrog pepsinogens.
 A;Reference number: JC7573; MUID:21064922; PMID:11134969
 A;Contents: Stomach
 A;Accession: JC7573
 A;Molecule type: mRNA
 A;Residues: 1-383 <IKU>
 A;Cross-references: DDBJ:AB045379
 A;Accession: PC7118
 A;Molecule type: protein
 A;Residues: 17-68 <IK2>
 C;Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like activity.
 C;Genetics:
 A;Gene: PgC
 C;Superfamily: pepsin
 C;Keywords: stomach; zymogen

Query Match 16.4%; Score 346.5; DB 2; Length 383;
 Best Local Similarity 29.9%; Pred. No. 8.3e-20;
 Matches 118; Conservative 60; Mismatches 124; Indels 93; Gaps 23;

QY	1	ALEPALASPAGAA	FLAMVDNLQGD	SGRGYYLEML	IGTPPQKLQIL	VDTGSSNFAV	AGTP	60
			:	:				
Db	55	AYEP-----	LSNYMDM-----	SYG	EISIGTPPQ	NFLVLFDTG	SSNLWVAST-	96
QY	61	HSYIDT-----	YDTERSSTY	RSKGF	DVTVKYTQGS	WTGFVGED	LV	113
		:	:	:		:	:	
Db	97	--YCQSQACT	NHPLFNPSQS	SSTYSSNQQQ	FSLQYGTG	SLTGILGYD	TVTIQ-----	145
QY	114	NIATIFESE	NFFL----	PG-----	IKWNGILGL	AYATLAKP	SSSLETFFD	200
		:	:	:		:	:	
Db	146	NVA--ISQQE	FGLSETEP	GTNFVYAQ	FDGILGLA	YPSIAVGG	AT--TVMQGM	200
QY	165	--VF	SMQMC	GAGLPVAG	SGTNGGSL	VLGGIEP	SLYKGD	222
		:	:			:	:	
Db	201	QPIFGFYLS	GQ-----	SSQNGGE	VAFGGVDQ	NYTGTQI	YWTPTSET	254
QY	223	GQSLNLD	CREYNAD	KAIVDSG	TLLRLPQK	VDAVVEA	VARASLI	282
		:	:	:		:	:	
Db	255	GQATGW-CS	Q--GCQA	IVDTGT	SLLTAPQ	SVFSSLI	QSIG-----	303
QY	283	WTNSETP	WSYFPK	ISIYLR	DENSSRS	FRITILP	QLYI-QP	337
		:	:		:		:	
Db	304	CSNIQN---	LPTISFTI---	SGVSFPLP--	PSAYVLQ	QSSG-----	YC-TIGIM	347
QY	338	PSTNA---	LVIGATV	MEGFYV	IFDRAQ	KRVGFA	AS	369
			:	:	:	:	:	
Db	348	PSQNGQPL	WILGDV	FLREYYS	VYDLGNN	QVGFATA		382

RESULT 7

A39314

gastricsin (EC 3.4.23.3) precursor - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 22-Jun-1999

C;Accession: A39314

R;Yakabe, E.; Tanji, M.; Ichinose, M.; Goto, S.; Miki, K.; Kurokawa, K.; Ito, H.; Kageyama, T.; Takahashi, K.

J. Biol. Chem. 266, 22436-22443, 1991

A;Title: Purification, characterization, and amino acid sequences of pepsinogens and pepsins from the esophageal mucosa of bullfrog (Rana catesbeiana).

A;Reference number: A39314; MUID:92042186; PMID:1939266

A;Accession: A39314

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-384 <YAK>

A;Cross-references: GB:M73750; NID:g213687; PIDN:AAA49530.1; PID:g213688

C;Superfamily: pepsin

C;Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match 16.1%; Score 339.5; DB 2; Length 384;

Best Local Similarity 27.5%; Pred. No. 3e-19;

Matches 108; Conservative 63; Mismatches 125; Indels 97; Gaps 17;

Qy	14	NFLAMVDNLQGD	SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDT-----	66
		:	: : : :	
Db	51	NFATAFEPLANYMDMSYYGEISIGTPPQNFLVLFD	TGSSNLWV---PSTYCQSQACTNHP	107
Qy	67	YFDTERSSTYRSKGF	DVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF	126
		: : :	: : : :	
Db	108	QFNPSQSSSYSSNQQQFSLQYGTGSLTGILGYDTVQIQ-----	NIA--ISQQEFGL	156
Qy	127	----PG-----	IKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPN--VFSMQMCGAGL	175
		: : : : :	: : : : :	
Db	157	SVTEPGTNFVYAQFDGILGLAYPSIAEGGAT--TVMQGM	I-QQNLINQPLFAFYLSG---	210
Qy	176	PVAGSGTNGGSLVLGGIEPSLYK	GDIWYTPIKEEWYYQIEILKLEIGGQSLNLD	235
		: : : : : : :	: : :	
Db	211	--QQNSQNGGEVAFGGVDQNYYS	GQIYWTPVTSETYWQIGIQGFSVNGQATGW-CSQ--G	265
Qy	236	DKAIVDSGTTLRLRPQKVFD	AVVEAVARASLIPEFSDGFWTGSQ-----	287
		: : : : : : :	: : :	
Db	266	CQGIVDTGTSLLTAPQSVFSSLMQSI-----	GAQQDQNGQYAVSCSNIQS	310
Qy	288	TPWSYFP-----	KISYLRDENS---SRSFRITILPQLYIQPMMGAGLNYECYRFGI	336
			: : : :	
Db	311	LPTISFTISGVSFPLPPSAYVLQQNSGYCTIGIMPTYLPSQNGQPLW-----		357
Qy	337	SPSTNALVIGATVMEGFYVIFDRAQKRVGFAAS		369
		: : : : : : : :		
Db	358	-----	ILGDVFLRQYYSVYDLGNNQVGFAAA	383

RESULT 8

B43356

gastricsin (EC 3.4.23.3) precursor - guinea pig

N;Alternate names: pepsin C

C;Species: *Cavia porcellus* (guinea pig)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
 C;Accession: B43356
 R;Kageyama, T.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Koiwai, O.;
 Tanji, M.; Yakabe, E.; Athauda, S.B.; Takahashi, K.
 J. Biol. Chem. 267, 16450-16459, 1992
 A;Title: Gastric procathepsin E and progastriksin from guinea pig. Purification,
 molecular cloning of cDNAs, and characterization of enzymatic properties, with
 special reference to procathepsin E.
 A;Reference number: A43356; MUID:92355614; PMID:1644829
 A;Accession: B43356
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-394 <KAG>
 A;Cross-references: GB:M88652; NID:g191296; PIDN:AAA37053.1; PID:g191297
 A;Note: sequence extracted from NCBI backbone (NCBIN:110805, NCBIP:110806)
 C;Superfamily: pepsin
 C;Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion;
 stomach

Query Match 15.4%; Score 324.5; DB 2; Length 394;
 Best Local Similarity 29.0%; Pred. No. 4.8e-18;
 Matches 107; Conservative 63; Mismatches 116; Indels 83; Gaps 18;

```

QY      30 YYLEMLIGTPPQKLQILVDTGSSNF-----AVAGTPHSYIDTYFDTERSSTYRSKGF 81
      |: :: :| | | | | | :| | | | | | :| | | | | | :| | | | | | :
Db      79 YFGQISLGTTPPQS FQVLFDTGSSNLWVPSVYCSSLACTTH----TRFNPRDSSTYVATDQ 134

QY      82 DVTVKYTQGSWTGFVGEDLVTI-----PK-GFNTSFLVNIATIFESENFFLPG-----IK 130
      ::::| | | | | | :| | | | | | :| | | | | | :| | | | | | :
Db     135 SFSLEYGTGSLTG VFGYDTMTIQDIQVPKQEFGLS-----ETE----PGSDFVYAE 181

QY     131 WNGILGLAYATLAKPSSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVAGS--GTNGGSL 187
      ::| | | | | | | :| | | | | | :| | | | | | :| | | | | | :
Db     182 FDGILGLGYPGLSEGGAT--TAMQGLLREGALSQSLFSVYL-----GSQQGSDEGQL 231

QY     188 VLGgiePSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTLL 247
      :| | | :| | | | | | :| | | | | | :| | | | | | :| | | | | | :
Db     232 ILGGVDESlytGDIYWTPVTQELYWQIGIEGFLIDGSASGWCSR---GCQGIVDTGTSL 288

QY     248 RLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYLRDENS SR 307
      :| | | :| | | | | | :| | | | | | :| | | | | | :| | | | | | :
Db     289 TVPSDYLSTLVQAIGAE--NEYGEYF-----VSCSSIQDLPTLTFVISGV----- 332

QY     308 SFRITILPQLYIQP-----MMGAGLNYECYRFGISPSTN--ALVIGATVMEGFYVIFDRA 360
      :| | | | | | :| | | | | | :| | | | | | :| | | | | | :
Db     333 --EFPLSPSAYILSGENYCMVGLESTY-----VSPGGGEPVWILGDVFLRSYYSVYDLA 384

QY     361 QKRVGFAAS 369
      | | | | | :
Db     385 NNRVGFATA 393
  
```

RESULT 9
 JC7575
 pepsinogen A - bullfrog
 C;Species: *Rana catesbeiana* (bullfrog)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C;Accession: JC7575
 R;Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.
 J. Biochem. 129, 147-153, 2001
 A;Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens, and molecular cloning of Xenopus and bullfrog pepsinogens.
 A;Reference number: JC7573; MUID:21064922; PMID:11134969
 A;Contents: Stomach
 A;Accession: JC7575
 A;Molecule type: mRNA
 A;Residues: 1-385 <IKU>
 A;Cross-references: DDBJ:AB045376
 C;Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like activity.
 C;Genetics:
 A;Gene: PgA
 C;Superfamily: pepsin
 C;Keywords: stomach; zymogen

Query Match 15.0%; Score 318; DB 2; Length 385;
 Best Local Similarity 28.2%; Pred. No. 1.5e-17;
 Matches 108; Conservative 65; Mismatches 136; Indels 74; Gaps 15;

```

Qy      4 PALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSY 63
      |:|| :|      : ||      | : : ||||| : : ||||| | | |
Db      55 PSLAQASG-----EPLQNYMDIEYFGTISIGTPPQSFTVIFDTGSSNLWV---PSVY 103

Qy      64 IDT-----YFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIA 116
      :      | : : |||::: |:::| || :||:| | | : | |
Db      104 CSSPACTNHMFNPQSSSTFQATNTPVSIQYGTGMSGFLGYDTVQVG---NIQITNQIF 160

Qy      117 TIFESE-NFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIP-NVFSMQMCGAG 174
      : :|| || :||||||: :|| || ||:: | || :||: :
Db      161 GLSQSEPGSFLYYSPFDGILGLAFPSLA--SSQATPVFDNMWNQGLIPQDLFSVYL---- 214

Qy      175 LPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYN 234
      : | :| : : ||:: | | |:: : | : | | : : ||| :
Db      215 ---SSQGQSGSFVLFGGVDTSYTGNLNVVPLTAETYWQITVDSISIGGQVIACS----G 267

Qy      235 ADKAIVDSGTLLRLPQKVFDVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFP 294
      : ||||:|:| | | : : | : : | : : | | | |
Db      268 SCSAIVDTGTSLLAGPSTPI-ANIQYYIGAN---QDSNGQYV---INCNNISNMPTVVFT 320

Qy      295 -----KISIIYLRDENSS--RSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALV 344
      | | :| | | : | | : | |
Db      321 INGVQYPLPASAYVRQSQQSCTSGFQAMNLP-----TSSGDLWI 359

Qy      345 IGATVMEGFYVIFDRAQKRVGEA 367
      :| : :||:|||| | |
Db      360 LGDVFIREFYYVVFDRANNYVAMA 382

```

RESULT 10
 A24608
 gastricsin (EC 3.4.23.3) precursor - rat
 N;Alternate names: pepsinogen C
 N;Contains: pepsin A (EC 3.4.23.1) precursor

C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Jun-1988 #sequence_revision 05-Aug-1994 #text_change 18-Jun-1999
 C;Accession: A33510; A24608; C22434; A05145; A61298
 R;Ishihara, T.; Ichihara, Y.; Hayano, T.; Katsura, I.; Sogawa, K.; Fujii-Kuriyama, Y.; Takahashi, K.
 J. Biol. Chem. 264, 10193-10199, 1989
 A;Title: Primary structure and transcriptional regulation of rat pepsinogen C gene.
 A;Reference number: A33510; MUID:89255508; PMID:2722863
 A;Accession: A33510
 A;Molecule type: DNA
 A;Residues: 1-392 <ISH>
 A;Cross-references: GB:M25985
 R;Ichihara, Y.; Sogawa, K.; Morohashi, K.; Fujii-Kuriyama, Y.; Takahashi, K.
 Eur. J. Biochem. 161, 7-12, 1986
 A;Title: Nucleotide sequence of a nearly full-length cDNA coding for pepsinogen of rat gastric mucosa.
 A;Reference number: A24608; MUID:87054020; PMID:3780741
 A;Accession: A24608
 A;Molecule type: mRNA
 A;Residues: 1-392 <ICH>
 A;Cross-references: GB:X04644; NID:g56880; PIDN:CAA28305.1; PID:g56881
 R;Ichihara, Y.; Sogawa, K.; Takahashi, K.
 J. Biochem. 98, 483-492, 1985
 A;Title: Isolation of human, swine, and rat prepepsinogens and calf preprochymosin, and determination of the primary structures of their NH2-terminal signal sequences.
 A;Reference number: A22434; MUID:86059312; PMID:2415509
 A;Accession: C22434
 A;Molecule type: protein
 A;Residues: 1-19,'X',21-23,'X',25-29 <IC2>
 R;Arai, K.M.; Muto, N.; Tani, S.; Akahane, K.
 Biochim. Biophys. Acta 788, 256-261, 1984
 A;Title: The N-terminal sequence of rat pepsinogen.
 A;Reference number: A05145; MUID:84257697; PMID:6743670
 A;Accession: A05145
 A;Molecule type: protein
 A;Residues: 17-30,'Q',32-102,'A',104-108,'L',110-112 <ARA>
 A;Experimental source: Wistar strain
 R;Ichihara, Y.; Sogawa, K.; Takahashi, K.
 J. Biochem. 92, 603-606, 1982
 A;Title: Rat gastric prepepsinogen: in vitro synthesis and partial amino-terminal signal sequence.
 A;Reference number: A61298; MUID:83030750; PMID:6182139
 A;Accession: A61298
 A;Molecule type: protein
 A;Residues: 1,'XX',4-6,'X',8-9,'X',11,'X',13-14,'XXX',18-19,'X',21,'X',23,'XX',26,'X' <IC3>
 C;Comment: This enzyme has more restricted specificity than pepsin A. It is the major form of pepsinogen in rat gastric mucosa.
 C;Genetics:
 A;Introns: 20/2; 73/3; 113/1; 152/3; 219/2; 259/2; 309/3; 342/3
 A;Note: there are at least two very similar genes for gastricsin in rat
 C;Superfamily: pepsin
 C;Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion; stomach
 F;1-16/Domain: signal sequence #status experimental <SIG>

QY 30 YYLEMLIGTPPQKLQILVDTGSSNFAVAG----TPHSYIDTYFDTERSSTYRSKGFDTV 85
 || : ||||| : : ||||| | : | : ||||| : || : : :
 Db 76 YYGTTISIGTPPQDFTVVFDTGSSNLWVPSVSTSPACQSHQMFNPSQSSTYKSTGQNLSI 135

QY 86 KYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFFLPGIKWNGILGLAYATLAKP 145
 | | | || | || : : | : : | | || : : : ||||| | : ||
 Db 136 HYGTDMEGTVGCDTVTVASLMDTNQLFGLST-SEPGQFFV-YVKFDGILGLGYPSLA-- 191

QY 146 SSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIWYT 204
 : : || : : : | : : : : | : ||| : | : | :
 Db 192 ADGITPVFDNMVNESLLEQNLFVSVYLSREPM-----GSMVVFGGIDESYFTGSINWI 243

QY 205 PIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVFDVAVVEAVARA 264
 | : : | : || : : : | : : : || : || : || : | : : ||
 Db 244 PVSYYQGYWQISMDSIIVNKQEIACS----SGCQAIIDTGTSLVAGPASDINDIQSAVG-- 297

QY 265 SLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIIYLRDENSRSFRITILPQLYIQPMMG 324
 | | | | | | | | : | : : : |
 Db 298 -----ANQNTYGEY-----SVNCSHILAMPDVVF--VIG 324

QY 325 AGLNY-----ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFA 367
 | : | | : | : : : | : : ||||| ||| |
 Db 325 -GIQYPVPALAYTEQNGQGTCMSSFQNSSADLWILGDVFIRVYYSIFDRANNRVGLA 380

RESULT 12

KHMSD

cathepsin D (EC 3.4.23.5) precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999

C;Accession: I48278; S14704; S12587

R;Hetman, M.; Perschl, A.; Saftig, P.; Von Figura, K.; Peters, C.

DNA Cell Biol. 13, 419-427, 1994

A;Title: Mouse cathepsin D gene: molecular organization, characterization of the promoter, and chromosomal localization.

A;Reference number: I48278; MUID:94280622; PMID:8011168

A;Accession: I48278

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-410 <RES>

A;Cross-references: EMBL:X68378; NID:g50302; PIDN:CAA48453.1; PID:g817945

R;Diedrich, J.F.; Staskus, K.A.; Retzel, E.F.; Haase, A.T.

Nucleic Acids Res. 18, 7184, 1990

A;Title: Nucleotide sequence of a cDNA encoding mouse cathepsin D.

A;Reference number: S14704; MUID:91088345; PMID:2263503

A;Accession: S14704

A;Molecule type: mRNA

A;Residues: 1-410 <DIE>

A;Cross-references: EMBL:X53337; NID:g50300; PIDN:CAA37423.1; PID:g50301

R;Grusby, M.J.; Mitchell, S.C.; Glimcher, L.H.

Nucleic Acids Res. 18, 4008, 1990

A;Title: Molecular cloning of mouse cathepsin D.

A;Reference number: S12587; MUID:90326544; PMID:2374732

A;Accession: S12587

A;Molecule type: mRNA

A;Residues: 1-410 <GRU>

A;Cross-references: EMBL:X52886; NID:g50298; PIDN:CAA37067.1; PID:g50299

A;Reference number: S13111; MUID:91057150; PMID:2243802
 A;Accession: S13111
 A;Molecule type: mRNA
 A;Residues: 1-407 <BIR>
 A;Cross-references: EMBL:X54467; NID:g55881; PIDN:CAA38349.1; PID:g55882
 R;Yonezawa, S.; Takahashi, T.; Wang, X.; Wong, R.N.S.; Hartsuck, J.A.; Tang, J.
 J. Biol. Chem. 263, 16504-16511, 1988
 A;Title: Structures at the proteolytic processing region of cathepsin D.
 A;Reference number: A92681; MUID:89034127; PMID:3182800
 A;Accession: C31918
 A;Molecule type: protein
 A;Residues: 134-162,'T',164-170 <YON>
 R;Fujita, H.; Tanaka, Y.; Noguchi, Y.; Kono, A.; Himeno, M.; Kato, K.
 Biochem. Biophys. Res. Commun. 179, 190-196, 1991
 A;Title: Isolation and sequencing of a cDNA clone encoding rat liver lysosomal
 cathepsin D and the structure of three forms of mature enzymes.
 A;Reference number: JQ1177; MUID:91354249; PMID:1883350
 A;Accession: JQ1177
 A;Molecule type: mRNA
 A;Residues: 1-14,'A',16-204,'N',206-261,'N',263-407 <FUJ>
 A;Accession: PQ0222
 A;Molecule type: protein
 A;Residues: 65-74;118-127;165-174 <FU2>
 A;Experimental source: liver
 C;Comment: Cathepsin D in rat liver lysosome occurs as a mixture of both a
 single chain form and two types of two chain forms.
 C;Function:
 A;Description: limited specificity endopeptidase
 A;Pathway: intracellular protein degradation
 C;Superfamily: pepsin
 C;Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein
 degradation
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-64/Domain: propeptide #status predicted <PRO>
 F;65-407/Product: cathepsin D, 43K single-chain form #status predicted <MAT>
 F;65-164/Product: (or 65-165) cathepsin D 12K light chain #status predicted
 <MA2>
 F;65-117/Product: cathepsin D 9K light chain #status predicted <MA4>
 F;118-407/Product: cathepsin D 34K heavy chain #status predicted <MA5>
 F;165-407/Product: (or 166-407) cathepsin D 30K heavy chain #status predicted
 <MA3>
 F;91-160,110-117,281-285,324-361/Disulfide bonds: #status predicted
 F;97,290/Active site: Asp #status predicted
 F;134,258/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.4%; Score 305; DB 1; Length 407;
 Best Local Similarity 29.4%; Pred. No. 1.8e-16;
 Matches 104; Conservative 61; Mismatches 143; Indels 46; Gaps 15;

Qy	30	YYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDT-----YFDTERSSTYRSKGFDV	83
		: :: : ::::	
Db	79	YYGEIGIGTPPQCFTVVFDTGSSNLWVPSIHCKLLDIACWVHHKYNSDKSSTYVKNGTSF	138
Qy	84	TVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATIFESENFFLPGI-----KWNGILGLA	138
		: : :: : :: : : : :: :	
Db	139	DIHYGSGSLSGYLSQD TVSVPCSDLGGIKVEKQIF-GEATKQPGVVFIAAKFDGILGMG	197

Qy 139 YATLAKPSSSLETFFDLSLVTQANI-PNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLY 197
 | :: : : ||:|: | : |:|| | :| || |:| | : |
 Db 198 YPFIS--VNKVLFPVFDNLMKQKLVEKNIFSFY-----LNRDPTGQPGGELMLGGTDSRY 250
 Qy 198 KGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVFD 257
 |:: | : : |:|: : :||:| : | | |: :|||:| |:| | | |
 Db 251 HGELSYLNVTRKAYWQVHMDQLEVGSE-LTL-CK--GGCEAIVDTGTSLLVGP---VDEV 303
 Qy 258 VEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQL 317
 | :| : : | | | : | | | : | :| : | :
 Db 304 KELQKAIGAVPLIQGEY----MIPC-----EKVSSLPIITFKLGGQN-----YELHPEK 348
 Qy 318 YIQPMMGAGLNYECYRF---GISPSTNAL-VIGATVMEGFYVIFDRAQKRVGFA 367
 || : || | | : | :| : :| :||| ||||
 Db 349 YILKVSQAGKTICLSGFMGMDIPPPSGPLWILGDVFIGCYTTFDREYNRVGFA 402

RESULT 14

REMSK

renin (EC 3.4.23.15) precursor, renal - mouse

N;Alternate names: angiotensin-forming enzyme; angiotensinogenase; renin 1

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999

C;Accession: A00989; S07636; A22766; A22058; I57576; A05137; JH0083

R;Holm, I.; Ollo, R.; Panthier, J.J.; Rougeon, F.

EMBO J. 3, 557-562, 1984

A;Title: Evolution of aspartyl proteases by gene duplication: the mouse renin gene is organized in two homologous clusters of four exons.

A;Reference number: A00989; MUID:84182525; PMID:6370686

A;Accession: A00989

A;Molecule type: DNA

A;Residues: 1-402 <HOL>

A;Cross-references: EMBL:X00850

R;Kim, W.S.; Murakami, K.; Nakayama, K.

Nucleic Acids Res. 17, 9480, 1989

A;Title: Nucleotide sequence of a cDNA coding for mouse Ren1 preprorenin.

A;Reference number: S07636; MUID:90067953; PMID:2685761

A;Accession: S07636

A;Molecule type: mRNA

A;Residues: 1-402 <KIM>

A;Cross-references: EMBL:X16642; NID:g53930; PIDN:CAA34636.1; PID:g53931

R;Mullins, J.J.; Burt, D.W.; Windass, J.D.; McTurk, P.; George, H.; Brammar, W.J.

EMBO J. 1, 1461-1466, 1982

A;Title: Molecular cloning of two distinct renin genes from the DBA/2 mouse.

A;Reference number: A90968; MUID:84207899; PMID:6327270

A;Accession: A22766

A;Molecule type: mRNA

A;Residues: 269-314,'D',316 <MUL>

R;Panthier, J.J.; Dreyfus, M.; Roux, D.T.L.; Rougeon, F.

Proc. Natl. Acad. Sci. U.S.A. 81, 5489-5493, 1984

A;Title: Mouse kidney and submaxillary gland renin genes differ in their 5' putative regulatory sequences.

A;Reference number: A22058; MUID:84298161; PMID:6089205

A;Accession: A22058

A;Molecule type: DNA

A;Residues: 1-30 <PAN>

R;Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.W.
Mol. Cell. Biol. 4, 2321-2331, 1984
A;Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analysis of 5'-proximal flanking regions.
A;Reference number: I57576; MUID:85085936; PMID:6392850
A;Accession: I57576
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <RES>
A;Cross-references: GB:K02800; NID:g200689; PIDN:AAA40044.1; PID:g200690
C;Comment: The only known function of renal renin is to release angiotensin I from angiotensinogen in the plasma, initiating a cascade of reactions that produces an elevation of blood pressure and increased sodium retention by the kidney.
C;Comment: Renal renin is synthesized by the juxtaglomerular cells of the kidney in response to decreased blood pressure and sodium concentration.
C;Genetics:
A;Gene: Ren-1
A;Introns: 31/2; 81/3; 123/1; 162/3; 228/2; 268/2; 316/3; 349/3
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; blood pressure control; glycoprotein; hydrolase; kidney; plasma
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-64/Domain: propeptide #status predicted <PRO>
F;65-402/Product: renin #status predicted <MAT>
F;69,139,320/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;102,287/Active site: Asp #status predicted

Query Match 14.4%; Score 304; DB 1; Length 402;
Best Local Similarity 29.0%; Pred. No. 2.1e-16;
Matches 108; Conservative 60; Mismatches 152; Indels 52; Gaps 17;

QY	6	LASPAGAA	FLAMVDNL	QGD	SGR	GYYLE	MLIG	TPP	QKL	QIL	VDT	GSS	NFA	VAG	TPH	SY--	63
			:			:		:	:		:						
Db	70	LTSPVVL	TNYL---	NTQ----	YYGEI	GIG	TPP	QTF	KVIF	DTGS	ANL	WVP	STK	CSRL	Y	119	
QY	64	----	IDTYF	DTERS	SSTYR	SKG	FDVT	VKY	TQGS	WTGF	VGED	LVT	IPK	GFNT	SFL	VNI	ATIF 119
		: :	:		:		:		:		:		:		:		
Db	120	LACGIH	SLYESS	DSSSY	MENG	SDFT	IIHY	GSGR	VKG	FLSQ	DSVT	TV--	GGIT	VTQT	FGE	VT	EL 178
QY	120	ESENF	FLPGI	KWNG	ILGL	AYAT	LAKP	SSS	LET	FFD	SLVT	QANI	-PN	VFS	MQM	CAG	LPVA 178
			:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Db	179	PLIPF	ML--	AKFD	GVLM	GF--	AQAV	GGV	TPV	FDH	ILSQ	GV	LKEE	VFS	VYY--	----	NR 228
QY	179	GSGT	NGG	SLVL	GGIE	PSLY	KGDI	WYT	PIKE	EWWW	QIEI	LKLE	IGG	QSL	NLD	CRE	YNADKA 238
				:	:	:	:	:	:	:	:	:	:	:	:	:	
Db	229	GSHLL	GGEV	VLGG	SDPQ	HYQG	NFHY	VSIS	KTD	SWQI	TMKG	VSVG	--S	TLL	C	EEG	CA--V 284
QY	239	IVDS	GTT	LLRL	PQKV	FD	AV	VEAV	-AR	ASLI	PEF	SDG	FWT	GSQ	LAC	WTN	SETPWSYFPKIS 297
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Db	285	VVD	TGSS	FIS	APT	SSL	KLIM	QAL	GAKE	KRI	EY--	----	VVNC	---	SQVP	--	TLPDIS 331
QY	298	IYLR	DEN	SSRS	FRIT	ILPQ	LYIQ	PM	MG	AGL-	NYE	CYR	FGIS	PST	NAL-	VIG	ATVMEGFYV 355
Db	332	FDL---	GGRAY	TL	SST	DYV	LQY	PNRR	DKL	CTLA	LHAM	DIP	PPTG	PV	VLG	ATFIR	KFYT 387

Qy 356 IFDRAQKRVGFA 367
||| |:|||
Db 388 EFDRHNNRIGFA 399

RESULT 15

JC7574

pepsinogen A - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001

C;Accession: JC7574; PC7119

R;Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.

J. Biochem. 129, 147-153, 2001

A;Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens, and molecular cloning of Xenopus and bullfrog pepsinogens.

A;Reference number: JC7573; MUID:21064922; PMID:11134969

A;Contents: Stomach

A;Accession: JC7574

A;Molecule type: mRNA

A;Residues: 1-384 <IKU>

A;Cross-references: DDBJ:AB045380

A;Accession: PC7119

A;Molecule type: protein

A;Residues: 16-35;57-76 <IK2>

C;Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like activity.

C;Genetics:

A;Gene: PgA

C;Superfamily: pepsin

C;Keywords: stomach; zymogen

Query Match 14.3%; Score 302; DB 2; Length 384;

Best Local Similarity 27.5%; Pred. No. 2.8e-16;

Matches 103; Conservative 71; Mismatches 144; Indels 56; Gaps 17;

Qy 4 PALASPAGAAANFLAMVDNLQDSGRGYYLEMLIGTPPQKLQILVDTGSSNEFAVAGTPHSY 63
| || : : || || : ||||| : : ||||| : | | | |
Db 54 PTLAQ-----SSAETLQNYMDIEYYGTISIGTPPQEFTVIFDTGSANLWV---PSVY 102
Qy 64 IDTY-----FDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIA 116
: | : : ||| : : | : : | || : || : | | : | :
Db 103 CSSQACSNHNRFNPQQSSTFQATNTPVSIQYGTGMSGFLGYD--TLQVG-NIQISNQMF 159
Qy 117 TIFESE-NFFLPGIKWNGILGLAYATLAKPSSSLETFDLSVTQANIP-NVFSMQMCGAG 174
: ||| || : ||||| : : | || || : : | || : || : :
Db 160 GLSESEPGSFLYYSPFDGILGLAFPSIA--SSQATPVFDNMWSQGLIPQNLFSVYL---- 213
Qy 175 LPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYN 234
: | | : : || : : | | : : | : | : : | | : | :
Db 214 ---SSDGQTGSYVLFGGVDNSYYSGSLNWWPLTAETYWQITLDSVVSINGQV--IACSQ-- 266
Qy 235 ADKAIVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFP 294
: : |||| : || : | : : || : : | : : | : | : | :
Db 267 SCQAIVDTGTSLMTGPSTPI-ANIQNYIGAS---QDSNGQYV---INCNNISNMPTIVF- 318
Qy 295 KISIYLRDENSSRSFRITILPQLYI-QPMMGAGLNYECYRFGISPSTNALVIGATVMEGF 353
: : : | | : | : : : | : : : : : :

Db 319 -----TINGVQYPLSPSAYVRQNQQGCSSGFQAMNLPN-SGDLWILGDVFIRQY 367
Qy 354 YVIFDRAQKRVGFA 367
: :|||| | |
Db 368 FTVFDRANNYVAIA 381

Search completed: March 4, 2004, 15:41:00
Job time : 23.0277 secs

OM protein - protein search, using sw model

Run on: March 4, 2004, 15:39:01 ; Search time 45.3511 Seconds
 (without alignments)
 1890.324 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
 Perfect score: 2113
 Sequence: 1 ALEPALASPAGAAANFLAMVD.....STEDVASNCVPAQSLSEPIL 406

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description
No.						

1	2113	100.0	481	14	US-10-106-698-6366	Sequence 6366, Ap
2	2113	100.0	518	9	US-09-794-927-2	Sequence 2, Appli
3	2113	100.0	518	9	US-09-795-847-2	Sequence 2, Appli
4	2113	100.0	518	9	US-09-794-743-2	Sequence 2, Appli
5	2113	100.0	518	9	US-09-794-748-2	Sequence 2, Appli
6	2113	100.0	518	9	US-09-794-925-2	Sequence 2, Appli
7	2113	100.0	518	9	US-09-215-450-19	Sequence 19, Appl
8	2113	100.0	518	9	US-09-681-442-2	Sequence 2, Appli
9	2113	100.0	518	9	US-09-978-295A-196	Sequence 196, App
10	2113	100.0	518	9	US-09-886-143-2	Sequence 2, Appli
11	2113	100.0	518	9	US-09-978-697-196	Sequence 196, App
12	2113	100.0	518	9	US-09-978-192A-196	Sequence 196, App
13	2113	100.0	518	9	US-09-999-832A-196	Sequence 196, App
14	2113	100.0	518	10	US-09-978-189-196	Sequence 196, App
15	2113	100.0	518	10	US-09-978-608A-196	Sequence 196, App
16	2113	100.0	518	10	US-09-978-585A-196	Sequence 196, App
17	2113	100.0	518	10	US-09-978-191A-196	Sequence 196, App
18	2113	100.0	518	10	US-09-978-403A-196	Sequence 196, App
19	2113	100.0	518	10	US-09-978-564A-196	Sequence 196, App
20	2113	100.0	518	10	US-09-999-833A-196	Sequence 196, App
21	2113	100.0	518	10	US-09-981-915A-196	Sequence 196, App
22	2113	100.0	518	10	US-09-978-824-196	Sequence 196, App
23	2113	100.0	518	10	US-09-918-585A-196	Sequence 196, App
24	2113	100.0	518	10	US-09-978-423A-196	Sequence 196, App
25	2113	100.0	518	10	US-09-978-193A-196	Sequence 196, App
26	2113	100.0	518	10	US-09-869-414-2	Sequence 2, Appli
27	2113	100.0	518	10	US-09-999-830A-196	Sequence 196, App
28	2113	100.0	518	10	US-09-978-757A-196	Sequence 196, App
29	2113	100.0	518	10	US-09-978-187B-196	Sequence 196, App
30	2113	100.0	518	10	US-09-548-366-2	Sequence 2, Appli
31	2113	100.0	518	10	US-09-978-643A-196	Sequence 196, App
32	2113	100.0	518	10	US-09-978-375A-196	Sequence 196, App
33	2113	100.0	518	10	US-09-978-298A-196	Sequence 196, App
34	2113	100.0	518	10	US-09-978-188A-196	Sequence 196, App
35	2113	100.0	518	10	US-09-978-681A-196	Sequence 196, App
36	2113	100.0	518	10	US-09-978-194A-196	Sequence 196, App
37	2113	100.0	518	10	US-09-999-829A-196	Sequence 196, App
38	2113	100.0	518	10	US-09-978-299A-196	Sequence 196, App
39	2113	100.0	518	10	US-09-978-544A-196	Sequence 196, App
40	2113	100.0	518	10	US-09-978-665A-196	Sequence 196, App
41	2113	100.0	518	10	US-09-978-802A-196	Sequence 196, App
42	2113	100.0	518	13	US-10-052-586-72	Sequence 72, Appl
43	2113	100.0	518	14	US-10-174-590-72	Sequence 72, Appl
44	2113	100.0	518	14	US-10-176-758-72	Sequence 72, Appl
45	2113	100.0	518	14	US-10-175-737-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
 US-10-106-698-6366
 ; Sequence 6366, Application US/10106698
 ; Publication No. US20030109690A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6366
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-6366

Query Match 100.0%; Score 2113; DB 14; Length 481;
Best Local Similarity 100.0%; Pred. No. 3.9e-203;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	26	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	85
Qy	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFE	120
Db	86	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFE	145
Qy	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	146	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	205
Qy	181	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	206	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	265
Qy	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	300
Db	266	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	325
Qy	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	326	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	385
Qy	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	386	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	431

RESULT 2

US-09-794-927-2

; Sequence 2, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:

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; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-2

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Query Match          100.0%; Score 2113; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 4.3e-203;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
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Db      63 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy      61 HSYIDTYFDTERSSTYRSKGFDTVYKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 HSYIDTYFDTERSSTYRSKGFDTVYKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

Qy     121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 242

Qy     181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 240
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Db     243 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 302

Qy     241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
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Db     303 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 362

Qy     301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

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Qy 361 QKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
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Db 423 QKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 3

US-09-795-847-2

; Sequence 2, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 518

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-795-847-2

Query Match 100.0%; Score 2113; DB 9; Length 518;

Best Local Similarity 100.0%; Pred. No. 4.3e-203;

Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
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Db 63 ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy 61 HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIATIFE 120
|||||
Db 123 HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIATIFE 182

Qy 121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
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Db 183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 242

Qy 181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 240
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 Qy 241 DSGTTLLRLPQKVFD AVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL 300
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 Db 303 DSGTTLLRLPQKVFD AVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL 362
 Qy 301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
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 Db 363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422
 Qy 361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 4

US-09-794-743-2

; Sequence 2, Application US/09794743

; Patent No. US20010021391A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280BC

; CURRENT APPLICATION NUMBER: US/09/794,743

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 518

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-794-743-2

Query Match 100.0%; Score 2113; DB 9; Length 518;

Best Local Similarity 100.0%; Pred. No. 4.3e-203;

Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	63		ALEPALASPAGAAFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
Qy	61		HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123		HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
Qy	121		SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183		SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
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Db	243		GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	302
Qy	241		DSGTTLLRLPQKVFD AVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	300
Db	303		DSGTTLLRLPQKVFD AVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL	362
Qy	301		RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363		RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
Qy	361		QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423		QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 5

US-09-794-748-2

; Sequence 2, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-2

Query Match 100.0%; Score 2113; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 4.3e-203;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      63 ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy      61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

Qy     121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
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Db     183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 242

Qy     181 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 302

Qy     241 DSGTTLRLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
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Db     303 DSGTTLRLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 362

Qy     301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
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Db     363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

Qy     361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468
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RESULT 6

US-09-794-925-2

; Sequence 2, Application US/09794925

; Patent No. US20020064819A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280HI

; CURRENT APPLICATION NUMBER: US/09/794,925

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 518
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-794-925-2

Query Match 100.0%; Score 2113; DB 9; Length 518;
 Best Local Similarity 100.0%; Pred. No. 4.3e-203;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
Qy	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
Qy	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
Qy	181	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV	302
Qy	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	362
Qy	301	RDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
Qy	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 7

US-09-215-450-19

; Sequence 19, Application US/09215450

; Patent No. US20020068278A1

; GENERAL INFORMATION:

; APPLICANT: Giese, Klaus

; APPLICANT: Xin, Hong

; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES

; FILE REFERENCE: 1451.100 / 210030.447
; CURRENT APPLICATION NUMBER: US/09/215,450
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 518
; TYPE: PRT
; ORGANISM: human
US-09-215-450-19

Query Match 100.0%; Score 2113; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 4.3e-203;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      63 ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy      61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
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Db     123 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

Qy     121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
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Db     183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 242

Qy     181 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 240
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Db     243 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 302

Qy     241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL 300
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Db     303 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYL 362

Qy     301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVM EGFYVIFDRA 360
          |||
Db     363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVM EGFYVIFDRA 422

Qy     361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI L 406
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Db     423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI L 468
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RESULT 8

US-09-681-442-2

; Sequence 2, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-2

Query Match 100.0%; Score 2113; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 4.3e-203;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
Qy	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
Qy	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
Qy	181	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV	302
Qy	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	362
Qy	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
Qy	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 9
US-09-978-295A-196
; Sequence 196, Application US/09978295A

; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/084598

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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match          100.0%; Score 2113; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 4.3e-203;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
        |||
Db      63 ALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy      61 HSYIDTYFDTERSSTYRSKGFVDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
        |||
Db      123 HSYIDTYFDTERSSTYRSKGFVDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

Qy      121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS 180
        |||
Db      183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS 242

Qy      181 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV 240
        |||
Db      243 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV 302

Qy      241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
        |||
Db      303 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 362

Qy      301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
        |||
Db      363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

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Qy 361 QKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIIL 406
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 Db 423 QKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIIL 468

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RESULT 10
US-09-886-143-2
; Sequence 2, Application US/09886143
; Patent No. US20020159991A1
; GENERAL INFORMATION:
; APPLICANT: Cordell, Barbara
; APPLICANT: Schimmoller, Frauke
; APPLICANT: Liu, Yu-Wang
; APPLICANT: Quon, Diana Hom
; TITLE OF INVENTION: Modulation of A Levels by
; TITLE OF INVENTION: Secretase BACE2
; FILE REFERENCE: SCIOS.022A
; CURRENT APPLICATION NUMBER: US/09/886,143
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/215,729
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-143-2

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Query Match      100.0%;  Score 2113;  DB 9;  Length 518;
Best Local Similarity 100.0%;  Pred. No. 4.3e-203;
Matches 406;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy	1	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
Qy	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
Qy	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPVAGS	242
Qy	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	302
Qy	241	DSGTLLRLRPQKVFDVAVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISIIYL	300
Db	303	DSGTLLRLRPQKVFDVAVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISIIYL	362
Qy	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422

QY 361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
|||||
Db 423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 11

US-09-978-697-196

; Sequence 196, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match          100.0%; Score 2113; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 4.3e-203;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 HSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
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Qy     121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
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Db     183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 242

Qy     181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 240
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RESULT 12

US-09-978-192A-196

; Sequence 196, Application US/09978192A

; Patent No. US20020177553A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
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 ; APPLICANT: Gao, Wei-Qiang
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 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C9
 ; CURRENT APPLICATION NUMBER: US/09/978,192A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085697

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Query Match          100.0%;  Score 2113;  DB 9;  Length 518;
Best Local Similarity 100.0%;  Pred. No. 4.3e-203;
Matches 406;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db     123 HSYIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

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 Db 243 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV 302
 QY 241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
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 Db 303 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 362
 QY 301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
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 Db 423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468

RESULT 13

US-09-999-832A-196

; Sequence 196, Application US/09999832A

; Publication No. US20020192706A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
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 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
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 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C63
 ; CURRENT APPLICATION NUMBER: US/09/999,832A

; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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Query Match          100.0%;  Score 2113;  DB 9;  Length 518;
Best Local Similarity 100.0%;  Pred. No. 4.3e-203;
Matches 406;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy	1	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
Qy	61	HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
Qy	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
Qy	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	302
Qy	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIYL	362
Qy	301	RDENSSRSFRITILPQLYIQPMAGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMAGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
Qy	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 14

US-09-978-189-196

; Sequence 196, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
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; PRIOR APPLICATION NUMBER: 60/079663
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; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2113; DB 10; Length 518;
Best Local Similarity 100.0%; Pred. No. 4.3e-203;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
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Db      63 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

Qy     61 HSYIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 HSYIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

Qy    121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFEFDLVTQANIPNVFSMQMCGAGLPVAGS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFEFDLVTQANIPNVFSMQMCGAGLPVAGS 242

Qy    181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 302

Qy    241 DSGTTLRLRPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 DSGTTLRLRPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIYL 362

Qy    301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
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Db    363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

Qy    361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
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Db    423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 468
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RESULT 15

US-09-978-608A-196

; Sequence 196, Application US/09978608A

; Publication No. US20030045462A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

```

; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 196
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-978-608A-196

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Query Match          100.0%; Score 2113; DB 10; Length 518;
Best Local Similarity 100.0%; Pred. No. 4.3e-203;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ALEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
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Db      63 ALEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122

QY      61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      123 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 182

QY      121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDLVTQANIPNVFSMQMCGAGLPVAGS 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      183 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDLVTQANIPNVFSMQMCGAGLPVAGS 242

QY      181 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      243 GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIV 302

QY      241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      303 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 362

QY      301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      363 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 422

QY      361 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIIL 406
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      423 QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIIL 468

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Search completed: March 4, 2004, 15:57:37
Job time : 46.3511 secs

OM protein - protein search, using sw model

Run on: March 4, 2004, 15:28:35 ; Search time 58.3085 Seconds
(without alignments)
2196.942 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
Perfect score: 2113
Sequence: 1 ALEPALASPAGAAANFLAMVD.....STEDVASNCVPAQSLSEPIL 406

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	2032	96.2	439	4	Q9H2V8	Q9h2v8 homo sapien
2	1962	92.9	514	11	Q9JL18	Q9jl18 mus musculu
3	1962	92.9	514	11	Q8C5E9	Q8c5e9 mus musculu
4	1957	92.6	514	11	Q8C793	Q8c793 mus musculu
5	1923	91.0	423	4	Q8N2D4	Q8n2d4 homo sapien
6	1801	85.2	468	4	Q9NZL2	Q9nzl2 homo sapien
7	1653	78.2	396	4	Q9NZL1	Q9nzl1 homo sapien
8	1486.5	70.4	500	13	Q7T0Y2	Q7t0y2 xenopus lae
9	1134	53.7	501	11	Q8C7R1	Q8c7r1 mus musculu
10	1132	53.6	532	4	Q9ULS1	Q9uls1 homo sapien
11	1131	53.5	501	11	Q8BQY4	Q8bqy4 mus musculu
12	1126	53.3	501	4	Q8IYC8	Q8iyc8 homo sapien
13	1017	48.1	255	11	Q9R1P7	Q9rlp7 mus musculu
14	997	47.2	467	11	Q8C4F4	Q8c4f4 mus musculu
15	614.5	29.1	267	11	Q9CUU5	Q9cuu5 mus musculu
16	461	21.8	213	4	Q9P0D2	Q9p0d2 homo sapien
17	385	18.2	244	5	Q8WQY9	Q8wqy9 aphrocallis
18	355	16.8	389	13	Q9W643	Q9w643 gallus gall
19	355	16.8	389	13	Q9PWK1	Q9pwk1 gallus gall
20	351	16.6	389	6	Q9GMY4	Q9gmy4 sorex ungui
21	348	16.5	389	6	Q9GMY3	Q9gmy3 rhinolophus
22	346.5	16.4	383	13	Q9DEC3	Q9dec3 xenopus lae
23	344	16.3	389	6	Q9GMY5	Q9gmy5 suncus muri
24	339.5	16.1	384	13	Q91322	Q91322 rana catesb
25	335.5	15.9	388	6	Q9GMY2	Q9gmy2 oryctolagus
26	334.5	15.8	391	5	Q9VKP6	Q9vkp6 drosophila
27	326	15.4	399	13	O93458	O93458 podarcis si
28	324.5	15.4	372	5	Q9VLK3	Q9vlk3 drosophila
29	324.5	15.4	383	13	Q9DE45	Q9de45 salvelinus
30	322.5	15.3	397	13	Q9W6D4	Q9w6d4 hynobius le
31	322	15.2	390	6	Q8SQ41	Q8sq41 canis famil
32	319.5	15.1	387	13	Q9DDV5	Q9ddv5 salvelinus
33	319	15.1	419	5	Q95VA2	Q95va2 clonorchis
34	318	15.0	385	13	Q9DEC4	Q9dec4 rana catesb
35	316	15.0	378	13	Q9PUR9	Q9pur9 pseudopleur
36	316	15.0	392	11	Q9D7R7	Q9d7r7 mus musculu
37	315	14.9	397	13	Q800A0	Q800a0 rana catesb
38	313.5	14.8	396	13	O93428	O93428 chionodraco
39	312.5	14.8	354	5	Q9GYX7	Q9gyx7 boophilus m
40	309	14.6	383	5	O76856	O76856 dictyosteli
41	302	14.3	384	13	Q9DEC2	Q9dec2 xenopus lae
42	302	14.3	398	13	P87370	P87370 oncorhynchu
43	295	14.0	376	13	Q9PUR8	Q9pur8 pseudopleur
44	295	14.0	387	6	Q9GMY8	Q9gmy8 sorex ungui
45	294	13.9	413	3	O14413	O14413 pichia angu

ALIGNMENTS

RESULT 1

Q9H2V8

ID Q9H2V8 PRELIMINARY; PRT; 439 AA.
AC Q9H2V8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE CDA13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pheochromocytoma;
 RA Li Y., Huang Q., Peng, y, Song H., Yu Y., Xu S., Ren S., Chen Z.,
 RA Han Z.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 DR EMBL; AF212252; AAG41783.1; -.
 DR HSSP; P00797; 2REN.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Aspartyl protease; Hydrolase; Protease.
 SQ SEQUENCE 439 AA; 48275 MW; 02EC0E0E50F11602 CRC64;

Query Match 96.2%; Score 2032; DB 4; Length 439;
 Best Local Similarity 100.0%; Pred. No. 4.3e-161;
 Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	18	MVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYR	77
Db	1	MVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYR	60
QY	78	SKGFDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENFFLPGIKWNGILGL	137
Db	61	SKGFDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENFFLPGIKWNGILGL	120
QY	138	AYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLY	197
Db	121	AYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLY	180
QY	198	KGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVFDVAV	257
Db	181	KGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVFDVAV	240
QY	258	VEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQL	317
Db	241	VEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQL	300
QY	318	YIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAIEIAGA	377
Db	301	YIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAIEIAGA	360
QY	378	AVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	361	AVSEISGPFSTEDVASNCVPAQSLSEPIL	389

RESULT 2

Q9JL18

ID Q9JL18 PRELIMINARY; PRT; 514 AA.
 AC Q9JL18;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aspartyl protease 1.
 GN BACE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choi D.K., Sugano S., Sakaki Y.;
 RT "Molecular characterization of the mouse Aspl gene, a homolog of the
 RT human ASP1 (Down Syndrome Region aspartyl protease).";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 DR EMBL; AF216310; AAF36599.1; -.
 DR HSSP; P00797; 2REN.
 DR MEROPS; A01.041; -.
 DR MGD; MGI:1860440; Bace2.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Aspartyl protease; Hydrolase; Protease.
 SQ SEQUENCE 514 AA; 55799 MW; A70725F2C1DF5B47 CRC64;

Query Match 92.9%; Score 1962; DB 11; Length 514;
 Best Local Similarity 91.6%; Pred. No. 3.8e-155;
 Matches 372; Conservative 15; Mismatches 15; Indels 4; Gaps 1;

QY 1 ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
 |||| |: |||||||||||||||||||||||||||||||||||||||||
 Db 63 ALEPVRAT----ANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKVQILVDTGSSNFAVAGAP 118
 QY 61 HSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE 120
 |||||||||:| |||| |||||||||||||||||||||||||||||||||:|||||||
 Db 119 HSYIDTYFDSESSSTYHSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNSSFLVNIATIFE 178
 QY 121 SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS 180
 |||||||||||||||||||| |||||||||||||||| || ||:|||||||||||||||
 Db 179 SENFFLPGIKWNGILGLAYAALAKPSSSLETFFDSLVAQAKIPDIFSMQMCGAGLPVAGS 238
 QY 181 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV 240
 |||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
 Db 239 GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQNLNLD CREYNADKAIV 298

QY 241 DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL 300
 |||||:|||||:|||||
 Db 299 DSGTTLLRLPQKVFDVAVVEAVARTSLIPEFSDGFWTGAQLACWTNSETPWAYFPKISIIYL 358
 QY 301 RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA 360
 ||||:|||||:|||||:|||||
 Db 359 RDENASRSFRITILPQLYIQPMMGAGFNYECYRFGISSSTNALVIGATVMEGFYVIFDRA 418
 QY 361 QKRVGF AASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL 406
 |:|||||:|||||:|||||
 Db 419 QRRVGF AAVSPCAIEIGTTVSEISGPFSTEDIASNCVPAQALNEPIL 464

RESULT 3

Q8C5E9

ID Q8C5E9 PRELIMINARY; PRT; 514 AA.
 AC Q8C5E9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-site APP-cleaving enzyme 2.
 GN BACE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK078770; BAC37384.1; -.
 DR MGD; MGI:1860440; Bace2.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 SQ SEQUENCE 514 AA; 55811 MW; CBB9237BB68A0B2E CRC64;

Query Match 92.9%; Score 1962; DB 11; Length 514;
 Best Local Similarity 91.6%; Pred. No. 3.8e-155;
 Matches 372; Conservative 15; Mismatches 15; Indels 4; Gaps 1;

QY 1 ALEPALAS PAGAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 60
 |||||:|||||:|||||
 Db 63 ALEPV RAT----ANFLAMVDNLQGDSGRGYYLEMLIGTPPQKVQILVDTGSSNFAVAGAP 118
 QY 61 HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATIFE 120

Db	119	HSYIDTYFDSESSSTYHSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNSSEFLVNIATIFE	178
Qy	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	179	SENFFLPGIKWNGILGLAYAALAKPSSSLETFDLSLVAQAKIPDIFSMQMCAGLPVAGS	238
Qy	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	240
Db	239	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIV	298
Qy	241	DSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSET'PWSYFPKISIYL	300
Db	299	DSGTTLLRLPQKVFD AVEAVARTSLIPEFSDGFWTGAQLACWTNSETPWAYFPKISIYL	358
Qy	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	359	RDENASRSFRITILPQLYIQPMMGAGFNYECYRFGISSSTNALVIGATVMEGFYVIFDRA	418
Qy	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	419	QRRVGFAVSPCAIEIEGTTVSEISGPFSTEDIASNCVPAQALNEPIL	464

RESULT 4

Q8C793

ID Q8C793 PRELIMINARY; PRT; 514 AA.
AC Q8C793;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-site APP-cleaving enzyme 2.
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK052309; BAC34931.1; -.
DR MGD; MGI:1860440; Bace2.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001969; Aspprotease_AS.
DR InterPro; IPR001461; Peptidase_A1.
DR InterPro; IPR009007; Pept_A_acid.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
SQ SEQUENCE 514 AA; 55871 MW; 8BF45E07B0990225 CRC64;

DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 423 AA; 46457 MW; 4D4839F2ED9C2CE1 CRC64;

Query Match 91.0%; Score 1923; DB 4; Length 423;
 Best Local Similarity 99.2%; Pred. No. 5.2e-152;
 Matches 370; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	34	MLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWT	93
Db	1	MLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWT	60
QY	94	GFVGEDLVTIPKGFNTSFLVNIATIFESENFFLPGIKWNGILGLAYATLAKPSSSLETFF	153
Db	61	GFVGEDLVTIPKGFNTSFLVNIATIFESGNFFLPGIQWNGILGLAYATLAKPSSSLETFF	120
QY	154	DSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQ	213
Db	121	DSLVTQANIPNVFSMQMRGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQ	180
QY	214	IEILKLEIGGQSLNLD CREYNADKAI VDSGTTLLRLPQKVFD AVEAVARASLIPEFSDG	273
Db	181	IEILKLEIGGQSLNLD CREYNADKAI VDSGTTLLRLPQKVFD AVEAVARASLIPEFSDG	240
QY	274	FWTGSQ LACWTNSETPWSYFPKIS IYLRDENSSRSFRITILPQLYIQPMMGAGLNYECYR	333
Db	241	FWTGSQ LACWTNSETPWSYFPKIS IYLRDENSSRSFRITILPQLYIQPMMGAGLNYECYR	300
QY	334	FGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA EIAGAAVSEISGPFSTEDVAS	393
Db	301	FGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA EIAGAAVSEISGPFSTEDVAS	360
QY	394	NCVPAQSLSEPIL	406
Db	361	NCVPAQSLSEPIL	373

RESULT 6

Q9NZL2

ID Q9NZL2 PRELIMINARY; PRT; 468 AA.
 AC Q9NZL2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aspartyl protease.
 GN BACE2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20422477; PubMed=10965118;
 RA Solans A., Estivill X., de La Luna S.;
 RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
 RT Alzheimer's amyloid precursor protein beta-secretase.";
 RL Cytogenet. Cell Genet. 89:177-184(2000).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 DR EMBL; AF188276; AAF35835.1; -.
 DR HSSP; P00797; 2REN.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Aspartyl protease; Hydrolase; Protease.
 SQ SEQUENCE 468 AA; 50324 MW; 717E0920126A0142 CRC64;

Query Match 85.2%; Score 1801; DB 4; Length 468;
 Best Local Similarity 87.7%; Pred. No. 9.3e-142;
 Matches 356; Conservative 0; Mismatches 0; Indels 50; Gaps 1;

QY	1	ALEPALASPAGAANFLAMVDNLQDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAANFLAMVDNLQDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
QY	61	HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFE	182
QY	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
QY	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	302
QY	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASL-----	328
QY	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	329	-----LYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	372
QY	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	373	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	418

RESULT 7

Q9NZL1

ID Q9NZL1 PRELIMINARY; PRT; 396 AA.
 AC Q9NZL1;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aspartyl protease.
 GN BACE2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422477; PubMed=10965118;
 RA Solans A., Estivill X., de La Luna S.;
 RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
 RT Alzheimer's amyloid precursor protein beta-secretase."
 RL Cytogenet. Cell Genet. 89:177-184(2000).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 DR EMBL; AF188277; AAF35836.1; -.
 DR HSSP; P00797; 2REN.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Aspartyl protease; Hydrolase; Protease.
 SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;

Query Match 78.2%; Score 1653; DB 4; Length 396;
 Best Local Similarity 100.0%; Pred. No. 1.7e-129;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
QY	61	HSYIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFE	182
QY	121	SEFFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SEFFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
QY	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	302
QY	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYL	362
QY	301	RDENSSRSFRITILPQ	316

RESULT 8

Q7TOY2

ID Q7TOY2 PRELIMINARY; PRT; 500 AA.
AC Q7TOY2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS *Xenopus laevis* (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;
OC Xenopodinae; *Xenopus*.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC055989; AAH55989.1; -.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54722 MW; 10F16756CAFD0B CRC64;

DR MGD; MGI:1346542; Bace.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 SQ SEQUENCE 501 AA; 55761 MW; B410DA8B64647663 CRC64;

Query Match 53.7%; Score 1134; DB 11; Length 501;
 Best Local Similarity 54.0%; Pred. No. 5.2e-86;
 Matches 209; Conservative 64; Mismatches 110; Indels 4; Gaps 2;

QY	9	PAGAA	FLAMVDNLQGD	SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPH	SYIDTYF	68
			:	:	:	:
Db	54	PGRRGSFVEMVDNLRGKSGQGYVEMTIGSP	QTLN	ILVDTGSSNFAVGAAPHPFLH	RY	113
QY	69	DTERSSTYRSKGF	DVTVKYTQGSWTG	FVGEDLVTIPKGFNTSFLVNIATIFESENFF	LP	128
		:	:	:	:	:
Db	114	QRQLSSTYRDLRKG	VYPYTQGWEGELGTD	LVSI	PHGPNVTVRANIAA	ITESDKFFING 173
QY	129	IKWNGILGLAYATLAKPSSSLETFFDS	SLVTQANIPNVFSMQMCGAGLPV---	AGSGTNGG		185
			:	:	:	:
Db	174	SNWEGILGLAYAEIARPD	SLEPFFDSLVKQTHIPNIFSLQLCGAGFPLNQTEALASVGG			233
QY	186	SLVLGGIEPSLYK	GDIWYTPIKEEWYYQIEILKLEIGGQSLNLD	CREYNADKAI	VDSGTT	245
			:	:	:	:
Db	234	SMIIGGIDHSLYTGSLWYTP	IRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTT			293
QY	246	LLRLPQKVFD	AVVEAVARASLIPEFSDGFWTGSQ	LACWTNSETPWSYFPKIS	IYLRDENS	305
			:	:	:	:
Db	294	NLRLPKKVFEAAVKS	IKAAASSTEKFPDGF	WLGEQLVCWQAGTTPWNIFPVISLYLMGEVT		353
QY	306	SRSFRITILPQ	LYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV			364
		:	:	:	:	:
Db	354	NQSFRITILPQQYLR	PVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRI			413
QY	365	GFAASPCA	EIAGAAVSEISGPFSTEDV			391
			:	:	:	:
Db	414	GFAVSACHVHDEFRTAA	VEGPFVTADM			440

RESULT 10

Q9ULS1

ID Q9ULS1 PRELIMINARY; PRT; 532 AA.
 AC Q9ULS1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein KIAA1149 (Fragment).
 GN KIAA1149.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20039618; PubMed=10574461;
 RA Hirosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
 RT "Characterization of cDNA clones selected by the GeneMark analysis
 RT from size-fractionated cDNA libraries from human brain.";
 RL DNA Res. 6:329-336(1999).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 DR EMBL; AB032975; BAA86463.2; -.
 DR HSSP; P56272; 1AM5.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 KW Hypothetical protein; Aspartyl protease; Hydrolase; Protease.
 FT NON_TER 1 1
 SQ SEQUENCE 532 AA; 58720 MW; 98B135D0D5FBD2E8 CRC64;

Query Match 53.6%; Score 1132; DB 4; Length 532;
 Best Local Similarity 54.0%; Pred. No. 8.3e-86;
 Matches 209; Conservative 65; Mismatches 109; Indels 4; Gaps 2;

QY	9	PAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYF	68
		: : : : : : : :	
Db	85	PGRRGSFVEMVDNLRGKSGQGYVEMTVGSPQTLNQLVDTGSSNFAVGAAPHPFLHRY	144
QY	69	DTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFPLPG	128
		: : : : : :	
Db	145	QRQLSSTYRDLRKGVPYPTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFING	204
QY	129	IKWNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPVAGS---GTNGG	185
		: : : : : : : : : : :	
Db	205	SNWEGILGLAYAEIARPDLSLEPFDSLVLKQTHVPLNLSLQLCGAGFPLNQSEVLASVGG	264
QY	186	SLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTT	245
		: : : : : : : : : : : : : : : : :	
Db	265	SMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTT	324
QY	246	LLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWNTNSETPWSYFPKISYLRDENS	305
		: : : : : : :	
Db	325	NLRLPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLYLMGEVT	384
QY	306	SRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV	364
		: : : : : : : : : : : : : : :	
Db	385	NQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRI	444
QY	365	GFAASPCAIEIAGAAVSEISGPFSTEDV	391
		: : :	
Db	445	GFAVSACHVHDEFRTAAVEGPFVTLDM	471

RESULT 11

Q8BQY4

ID Q8BQY4 PRELIMINARY; PRT; 501 AA.
 AC Q8BQY4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-site APP cleaving enzyme.
 GN BACE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK046175; BAC32620.1; -.
 DR MGD; MGI:1346542; Bace.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 SQ SEQUENCE 501 AA; 55816 MW; C0855513145E024E CRC64;

Query Match 53.5%; Score 1131; DB 11; Length 501;
 Best Local Similarity 53.7%; Pred. No. 9.2e-86;
 Matches 208; Conservative 65; Mismatches 110; Indels 4; Gaps 2;

QY 9 PAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYF 68
 | :|: |||||:| ||:||||:| :|:||| | ||||| ||||| || :| :|
 Db 54 PGRRGSEFVEMVDNLRGKSGQGYVEMTVGSPQTLNILVDTGSSNFAVGAAPHPFLHRY 113
 QY 69 DTERSSTYRSKGFDTVKYTGGSWTGFGEDLVTIPKGFNTSFLVNIATIFESENFPLPG 128
 : ||||| | | |||| | | :| |||:|| | | : ||| | ||: ||: |
 Db 114 QRQLSSTYRDLRKGVPYPTQGKWEDELGTDLVSIHPGNVTVRANIAAITESDKFFING 173
 QY 129 IKWNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPV---AGSGTNGG 185
 | ||||| ||:| ||| ||||| | :|||:||:|:|||| |: : ||
 Db 174 SNWEGILGLAYAEIARPDDSLEPFDSLQTHIPNIFSLQLCGAGFPLNQTEALASVGG 233
 QY 186 SLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTT 245
 |:::||||: ||| | :|||||: ||||:| :::|| || | :||:|||| ||:|||||||
 Db 234 SMIIGGIDHSlyTGRLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDKSIVDSGTT 293
 QY 246 LLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENS 305
 ||||:||||:| |::: || :| |||| | || || ||||: || ||:|| | :
 Db 294 NLRLPKKVFEAAVKSIIKAASSTEKFPDGEQVLCWQAGTTPWNIFPVISLYLMGEVT 353

Qy 306 SRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV 364
 :||| ||||| |::| : :||:| :| |: |::| :||| |||||: |||: ||:
 Db 354 NQSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRI 413

Qy 365 GFAASPCAIEIAGAAVSEISGPFSTEDV 391
 ||| | | : : ||| | |:
 Db 414 GFAVSACHVHDEFRTAAVEGPFVVTADM 440

RESULT 12

Q8IYC8

ID Q8IYC8 PRELIMINARY; PRT; 501 AA.
 AC Q8IYC8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-site APP-cleaving enzyme.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC036084; AAH36084.1; -.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 SQ SEQUENCE 501 AA; 55824 MW; 768595CF5517EFB7 CRC64;

Query Match 53.3%; Score 1126; DB 4; Length 501;
 Best Local Similarity 53.7%; Pred. No. 2.4e-85;
 Matches 208; Conservative 65; Mismatches 110; Indels 4; Gaps 2;

QY 9 PAGAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYF 68
 | :|: |||||:| ||:||||:| :|:||| | ||||| ||||| || :|:
 Db 54 PGRRGSEFVEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFAVGAAPHPFLHRY 113

QY 69 DTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFFLP 128
 : |||| | | |||| | | :| |||:| | | : ||| | ||: ||: |
 Db 114 QRQLFSTYRDLRKGVPYPTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFING 173

QY 129 IKWNGILGLAYATLAKPSSSLETFFDLSVTQANIPNVFSMQMCGAGLPVAGS---GTNGG 185
 | ||||| ||:| ||| ||||| | :||:| |:| ||| | : | : ||
 Db 174 SNWEGILGLAYAEIARPDDSLEPFDFSLVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGG 233

QY 186 SLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTT 245
 |:::| | | | :|||: ||||: |::| | | | :||:| | | :||| |||
 Db 234 SMIIGGIDHSLYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTT 293

QY 246 LLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENS 305
 ||||:||||:| |::: || :| |||| | || || |||: || ||:| | :
 Db 294 NLRLPKKVFEAAVKSIAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVT 353
 QY 306 SRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV 364
 ::||||||||| |::|: : :||:| || |: |::| :|||||:||||:|:
 Db 354 NQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRI 413
 QY 365 GFAASPCAIEIAGAAVSEISGPFSTEDV 391
 ||| | | : : ||| | |:
 Db 414 GFAVSACHVHDEFRTAAVEGPFVTLDM 440

RESULT 13

Q9R1P7

ID Q9R1P7 PRELIMINARY; PRT; 255 AA.
 AC Q9R1P7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aspartyl protease (Fragment).
 GN BACE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Accarino M., Fumagalli P., Taramelli R., Ottolenghi S.;
 RT "Cloning of a gene from chromosome 21 Down Region encoding a potential
 RT transmembrane protease."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF051150; AAD45964.1; -.
 DR MEROPS; A01.041; -.
 DR MGD; MGI:1860440; Bace2.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 KW Protease.
 FT NON_TER 1 1
 SQ SEQUENCE 255 AA; 28685 MW; 53DE317815996D63 CRC64;

Query Match 48.1%; Score 1017; DB 11; Length 255;
 Best Local Similarity 92.2%; Pred. No. 1.1e-76;
 Matches 189; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 202 WYTPIKEEWYYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLRLPQKVFDVAVVEAV 261
 |||||||||||||||||||||:|||||||||||||||||||||||||||
 Db 1 WYTPIKEEWYYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLRLPQKVFDVAVVEAV 60
 QY 262 ARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENS SRSFRITILPQLYIQP 321
 || |||||||||||||||:|||||||||||||:|||||||||||||
 Db 61 ARTSLIPEFSDGFWTGAQLACWTNSETPWAYFPKISYLRDENASRSFRITILPQLYIQP 120

```
Qy      322 MMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGF AASPCAETIAGAAVSE 381  
        ||||| ||||||||| | : ||||| : ||||| ||||| | ||  
Db      121 MMGAGFNYECYRFGISSSTNALVIGATVMEGFYVVF DRAQRRVGFAVSPCAEIEGTTVSE 180  
  
Qy      382 ISGPFSTEDVASNCVPAQSLSEPIL 406  
        ||||||| : ||||||| : |: |||||  
Db      181 ISGPFSTEDIASNCVPAQALNEPIL 205
```

RESULT 14

```
Q8C4F4
ID      Q8C4F4          PRELIMINARY;          PRT;      467 AA.
AC      Q8C4F4;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Beta-site APP cleaving enzyme.
GN      BACE.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX      MEDLINE=22354683; PubMed=12466851;
RA      The FANTOM Consortium,
RA      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
DR      EMBL; AK082317; BAC38462.1; -.
DR      MGD; MGI:1346542; Bace.
DR      GO; GO:0004194; F:pepsin A activity; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR001969; Aspprotease_AS.
DR      InterPro; IPR001461; Peptidase_A1.
DR      InterPro; IPR009007; Pept_A_acid.
DR      Pfam; PF00026; asp; 1.
DR      PRINTS; PR00792; PEPSIN.
DR      PROSITE; PS00141; ASP_PROTEASE; 1.
SQ      SEQUENCE      467 AA;  52063 MW;  31AB674FF1843652 CRC64;
```

Query Match 47.2%; Score 997; DB 11; Length 467;
Best Local Similarity 48.1%; Pred. No. 1.3e-74;
Matches 186; Conservative 59; Mismatches 104; Indels 38; Gaps 3;

Qy	9	PAGAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYF	68
		: : : : : : : : :	
Db	54	PGRRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTNLILVDTGSSNFAVGAAHPHFLHRY	113
Qy	69	DTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVN IATIFESENFFLPG	128
		: : : : : :	
Db	114	QRQLSSTYRDLRKGVYPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFING	173
Qy	129	IKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV---AGSGTNGG	185

Db	174	SNWEGILGLAYAEIARPDSDLVVKQTHIPNIFSLQLCGAGFPLNQTEALASVGG	233
Qy	186	SLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTT	245
Db	234	SMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKE-----	280
Qy	246	LLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENS	305
Db	281	-----TEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVT	319
Qy	306	SRSFRITILPQLYIQPMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV	364
Db	320	NQSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRI	379
Qy	365	GFAASPCAIEIAGAAVSEISGPFSTEDV	391
Db	380	GFAVSACHVHDEFRTAAVEGPFVTADM	406

RESULT 15

Q9CUU5

ID Q9CUU5 PRELIMINARY; PRT; 267 AA.

AC Q9CUU5;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Adult male brain cDNA, RIKEN full-length enriched library,

DE clone:3526402A15 product:beta-site APP cleaving enzyme, full insert

DE sequence (Fragment).

GN BACE.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Brain;

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

RA Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 DR EMBL; AK014390; BAB29317.2; -.
 DR MGD; MGI:1346542; Bace.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 267 AA; 30333 MW; 9413EB4530AB63B0 CRC64;

Query Match 29.1%; Score 614.5; DB 11; Length 267;
 Best Local Similarity 52.4%; Pred. No. 4.9e-43;
 Matches 108; Conservative 41; Mismatches 56; Indels 1; Gaps 1;

QY 187 LVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDS GTTL 246
 ::|||: ||| | :||||: ||||: |::|| || | :||: ||| ||:|||||
 Db 1 MIIGGIDHSLYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYDKSIVDS GTTN 60

Qy	247	LRLPQKVFD	AVVEAVARASLIPEFS	DGFWTGSQ	LACWTNSETPWSY	FPKIS	SIYLRDENS	SS	306
		:	:	:	:	:	:	:	
Db	61	LRLPKKVFEA	AVKSIKAASSTEK	FPDGF	WLGEQLVCWQ	AGTTPWNIF	FPVISLYLM	GEVTN	120
Qy	307	RSFRITILP	QLYIQPMMGAG	LN-ECYR	FGISPSTNAL	VIGATVMEG	FYVIFDRAQ	KRVG	365
		:	:	:	:	:	:	:	
Db	121	QSFRITILP	QQYLRPVEDV	ATSQDDCYK	FAVSQSSTG	TVMGAVIMEG	FYVVFDRAR	KRIG	180
Qy	366	FAASPCA	EIAGAAVSEIS	GPSTEDV					391
			:	:					
Db	181	FAVSACHV	HDEFRTAAVEG	PFVTADM					206

Search completed: March 4, 2004, 15:38:53
Job time : 59.3085 secs

OM protein - protein search, using sw model

Run on: March 4, 2004, 15:22:30 ; Search time 12.9574 Seconds
 (without alignments)
 1631.532 Million cell updates/sec

Title: US-09-668-314C-2_COPY_63_468
 Perfect score: 2113
 Sequence: 1 ALEPALASPAGAAANFLAMVD.....STEDVASNCVPAQSLSEPIL 406

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2113	100.0	518	1	BAE2_HUMAN	Q9y5z0 homo sapien
2	1134	53.7	501	1	BACE_RAT	P56819 rattus norv
3	1133	53.6	501	1	BACE_MOUSE	P56818 mus musculu
4	1132	53.6	501	1	BACE_HUMAN	P56817 homo sapien
5	359.5	17.0	377	1	PEPC_MACFU	P03955 macaca fusc
6	351.5	16.6	388	1	PEPC_CALJA	Q9n2d3 callithrix
7	350.5	16.6	388	1	PEPC_HUMAN	P20142 homo sapien
8	324.5	15.4	394	1	PEPC_CAVPO	Q64411 cavia porce
9	313	14.8	392	1	PEPC_RAT	P04073 rattus norv
10	311	14.7	396	1	CATD_CLUHA	Q9dex3 clupea hare
11	306.5	14.5	383	1	PEPE_CHICK	P16476 gallus gall
12	306.5	14.5	410	1	CATD_MOUSE	P18242 mus musculu
13	305	14.4	407	1	CATD_RAT	P24268 rattus norv
14	304	14.4	402	1	RENI_MOUSE	P06281 mus musculu
15	302	14.3	324	1	PEP1_GADMO	P56272 gadus morhu
16	302	14.3	405	1	CARP_YEAST	P07267 saccharomyc
17	301.5	14.3	398	1	CATE_RAT	P16228 rattus norv

18	300.5	14.2	397	1	CATE_MOUSE	P70269	mus musculu
19	298.5	14.1	412	1	CATD_HUMAN	P07339	homo sapien
20	297	14.1	387	1	PEP2_RABIT	P27821	oryctolagus
21	297	14.1	388	1	PEPA_HUMAN	P00790	homo sapien
22	296	14.0	398	1	CATD_CHICK	Q05744	gallus gall
23	296	14.0	401	1	RENS_MOUSE	P00796	mus musculu
24	294	13.9	388	1	PEP2_MACFU	P27677	macaca fusc
25	294	13.9	400	1	RENI_SHEEP	P52115	ovis aries
26	293	13.9	387	1	PEP4_RABIT	P28713	oryctolagus
27	291	13.8	388	1	PEP4_MACFU	P27678	macaca fusc
28	291	13.8	406	1	RENI_HUMAN	P00797	homo sapien
29	291	13.8	406	1	RENI_PANTR	P60016	pan troglod
30	290.5	13.7	396	1	CATE_RABIT	P43159	oryctolagus
31	290	13.7	402	1	RENI_RAT	P08424	rattus norv
32	289	13.7	387	1	PEP3_RABIT	P27822	oryctolagus
33	288	13.6	387	1	PEP1_RABIT	P28712	oryctolagus
34	288	13.6	388	1	PEP1_MACFU	P03954	macaca fusc
35	287.5	13.6	509	1	APR1_ORYSA	Q42456	oryza sativ
36	287	13.6	367	1	PEPA_CHICK	P00793	gallus gall
37	287	13.6	391	1	CATE_CAVPO	P25796	cavia porce
38	287	13.6	396	1	CATE_HUMAN	P14091	homo sapien
39	286	13.5	388	1	PEPA_MACMU	P11489	macaca mula
40	285.5	13.5	387	1	PEPA_CALJA	Q9n2d4	callithrix
41	285.5	13.5	388	1	PAG_HORSE	Q28389	equus cabal
42	284.5	13.5	386	1	PEPA_PIG	P00791	sus scrofa
43	283.5	13.4	390	1	CATD_BOVIN	P80209	bos taurus
44	283	13.4	388	1	PEPF_RABIT	P27823	oryctolagus
45	282.5	13.4	381	1	CHYM_SHEEP	P18276	ovis aries

ALIGNMENTS

RESULT 1
 BAE2_HUMAN
 ID BAE2_HUMAN STANDARD; PRT; 518 AA.
 AC Q9Y5Z0; Q9UJT6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Beta secretase 2 precursor (EC 3.4.23.45) (Beta-site APP-cleaving
 DE enzyme 2) (Aspartyl protease 1) (Asp 1) (ASP1) (Membrane-associated
 DE aspartic protease 1) (Memapsin-1) (Down region aspartic protease).
 GN BACE2 OR ASP21.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057170; PubMed=10591213;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
 RA Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomasselli A.G., Parodi L.A., Henrikson R.L., Gurney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease
 RT beta-secretase activity."
 RL Nature 402:533-537(1999).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Xin H., Stephans J.C., Duan X., Harrowe G., Kim E., Grieshammer U.,
 RA Giese K.;
 RT "Identification of a novel aspartic-like protease differentially
 RT expressed in human breast cancer cell lines.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.;
 RT "Cloning of a gene from chromosome 21 Down region encoding a potential
 RT transmembrane aspartyl protease.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Solans A., Estivill X., de la Luna S.;
 RT "Cloning of a novel mammalian aspartyl protease.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20120043; PubMed=10656250;
 RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
 RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
 RT "Identification of a novel aspartic proteinase (Asp 2) as
 RT beta-secretase.";
 RL Mol. Cell. Neurosci. 14:419-427(1999).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20144060; PubMed=10677483;
 RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
 RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
 RT beta-amyloid precursor protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20289799; PubMed=10830953;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
 RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
 RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
 RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
 RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehrach H., Reinhardt R., Yaspo M.-L.;
 RT "The DNA sequence of human chromosome 21.";
 RL Nature 405:311-319(2000).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP CHARACTERIZATION.
 RX MEDLINE=22088158; PubMed=12093293;
 RA Turner R.T. III, Loy J.A., Nguyen C., Devasamudram T., Ghosh A.K.,
 RA Koelsch G., Tang J.;
 RT "Specificity of memapsin 1 and its implications on the design of
 RT memapsin 2 (beta-secretase) inhibitor selectivity.";
 RL Biochemistry 41:8742-8746(2002).
 CC -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; AF200342; AAF17078.1; -.
 DR EMBL; AF117892; AAD45240.1; -.
 DR EMBL; AF050171; AAD45963.1; -.
 DR EMBL; AF178532; AAF29494.1; -.
 DR EMBL; AF204944; AAF26368.1; -.
 DR EMBL; AF200192; AAF13714.1; -.
 DR EMBL; AL163284; CAB90458.1; -.
 DR EMBL; AL163285; CAB90554.1; -.
 DR EMBL; BC014453; AAH14453.1; -.
 DR HSSP; P00797; 2REN.
 DR MEROPS; A01.041; -.
 DR Genew; HGNC:934; BACE2.
 DR MIM; 605668; -.
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; TAS.
 DR GO; GO:0006464; P:protein modification; TAS.

DR GO; GO:0009306; P:protein secretion; TAS.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 ? POTENTIAL.
 FT CHAIN ? 518 BETA SECRETASE 2.
 FT DOMAIN 21 473 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 474 494 POTENTIAL.
 FT DOMAIN 495 518 CYTOPLASMIC (POTENTIAL).
 FT ACT_SITE 110 110 BY SIMILARITY.
 FT ACT_SITE 303 303 BY SIMILARITY.
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 36 36 A -> T (IN REF. 6).
 SQ SEQUENCE 518 AA; 56180 MW; 2E903150823760D3 CRC64;

Query Match 100.0%; Score 2113; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 1.6e-153;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	60
Db	63	ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
QY	61	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATIFE	120
Db	123	HSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATIFE	182
QY	121	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	180
Db	183	SENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS	242
QY	181	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	240
Db	243	GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIV	302
QY	241	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDFGTGSQLACWTNSETPWSYFPKISIIYL	300
Db	303	DSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDFGTGSQLACWTNSETPWSYFPKISIIYL	362
QY	301	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	360
Db	363	RDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRA	422
QY	361	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	406
Db	423	QKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIL	468

RESULT 2

BACE_RAT

ID BACE_RAT STANDARD; PRT; 501 AA.

AC P56819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Beta-secretase precursor (EC 3.4.23.46) (Beta-site APP cleaving
 DE enzyme) (Beta-site amyloid precursor protein cleaving enzyme)
 DE (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
 DE protease 2) (Memapsin-2).
 GN BACE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.;
 RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).
 CC -!- FUNCTION: Responsible for the proteolytic processing of the
 CC amyloid precursor protein (APP). Cleaves at the amino terminus of
 CC the A-beta peptide sequence, between residues 671 and 672 of APP,
 CC leads to the generation and extracellular release of beta-cleaved
 CC soluble APP, and a corresponding cell-associated carboxy-terminal
 CC fragment which is later release by gamma-secretase (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; AF190727; AAF04144.1; -.
 DR HSSP; P32329; 1YPS.
 DR MEROPS; A01.004; -.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal.
 FT SIGNAL 1 21 POTENTIAL.

FT	PROPEP	22	45	POTENTIAL.
FT	CHAIN	46	501	BETA-SECRETASE.
FT	DOMAIN	22	457	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	458	478	POTENTIAL.
FT	DOMAIN	479	501	CYTOPLASMIC (POTENTIAL).
FT	ACT_SITE	93	93	BY SIMILARITY.
FT	ACT_SITE	289	289	BY SIMILARITY.
FT	DISULFID	216	420	BY SIMILARITY.
FT	DISULFID	278	443	BY SIMILARITY.
FT	DISULFID	330	380	BY SIMILARITY.
FT	CARBOHYD	153	153	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	172	172	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	223	223	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	354	354	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	501 AA; 55806 MW; 24B445BC8BE87DE3 CRC64;		

Query Match 53.7%; Score 1134; DB 1; Length 501;
 Best Local Similarity 53.7%; Pred. No. 6e-79;
 Matches 208; Conservative 65; Mismatches 110; Indels 4; Gaps 2;

Qy	9	PAGAAFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYF	68
Db	54	PGRRGSEFVEMVDNLRGKSGQGYVEMTVGSPQTLNVLVDTGSSNFAVGAAPHPFLHRY	113
Qy	69	DTERSSTYRSKGFVDVTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFLLPG	128
Db	114	QRQLSSTYRDLRKSVPYPTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFING	173
Qy	129	IKWNGILGLAYATLAKPSSSLETFFDLSVTQANIPNVFSMQMCGAGLPV---AGSGTNGG	185
Db	174	SNWEGILGLAYAEIARPDSDLFPFDLSLVKQTHIPNIFSLQLCGAGFPLNQTEALASVGG	233
Qy	186	SLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLDREYNADKAIVDSGTT	245
Db	234	SMIIGGIDHSLYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTT	293
Qy	246	LLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENS	305
Db	294	NLRLPKKVFEAAVKSIAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLYLMGEVT	353
Qy	306	SRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV	364
Db	354	NQSFRTILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRI	413
Qy	365	GFAASPCAELIAGAAVSEISGPFSTEDV	391
Db	414	GFAVSACHVHDEFRTAAVEGPFVTADM	440

RESULT 3

BACE_MOUSE

ID	BACE_MOUSE	STANDARD;	PRT;	501 AA.
AC	P56818;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Beta-secretase precursor (EC 3.4.23.46) (Beta-site APP cleaving			

DE enzyme) (Beta-site amyloid precursor protein cleaving enzyme)
 DE (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
 DE protease 2) (Memapsin-2).
 GN BACE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.;
 RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).
 RN [2]
 RP REVISIONS TO 6 AND 81-87.
 RA Bennett B.D., Vassar R., Citron M.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057170; PubMed=10591213;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
 RA Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease
 RT beta-secretase activity.";
 RL Nature 402:533-537(1999).
 CC -!- FUNCTION: Responsible for the proteolytic processing of the
 CC amyloid precursor protein (APP). Cleaves at the amino terminus of
 CC the A-beta peptide sequence, between residues 671 and 672 of APP,
 CC leads to the generation and extracellular release of beta-cleaved
 CC soluble APP, and a corresponding cell-associated carboxy-terminal
 CC fragment which is later release by gamma-secretase (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF190726; AAF04143.2; -.
 DR EMBL; AF200346; AAF17082.1; -.
 DR HSSP; P56272; 1AM5.

DR MEROPS; A01.004; -.
 DR MGD; MGI:1346542; Bace.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 45 POTENTIAL.
 FT CHAIN 46 501 BETA-SECRETASE.
 FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 458 478 POTENTIAL.
 FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
 FT ACT_SITE 93 93 BY SIMILARITY.
 FT ACT_SITE 289 289 BY SIMILARITY.
 FT DISULFID 216 420 BY SIMILARITY.
 FT DISULFID 278 443 BY SIMILARITY.
 FT DISULFID 330 380 BY SIMILARITY.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 501 AA; 55747 MW; C085A013145E474E CRC64;

Query Match 53.6%; Score 1133; DB 1; Length 501;
 Best Local Similarity 53.7%; Pred. No. 7.1e-79;
 Matches 208; Conservative 65; Mismatches 110; Indels 4; Gaps 2;

QY 9 PAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSHYIDTYF 68
 | :|: ||||:| ||:||||:| :|:|||| | ||||| ||||| || :|: |:
 Db 54 PGRRGSFVEMVDNLRGKSGQGYVEMTVGSPQTLNILVDTGSSNFAVGAAPHPFLHRY 113
 QY 69 DTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFFLP 128
 : ||||| | | |||| | | :| |||:| | | : ||| | ||: ||: |
 Db 114 QRQLSSTYRDLRKG VYVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFF 173
 QY 129 IKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV---AGSGT 185
 | ||||| ||| :|:| ||| ||||| | :|||:| |:| ||| | : ||
 Db 174 SNWEGILGLAYAEIARPDSDLFFDSL VKQTHIPNIFSLQLCGAGFPLNQTEALASV 233
 QY 186 SLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDS 245
 |:::| | | | :| | | | :| | | | :| | | | :| | | | :| | | |
 Db 234 SMIIGGIDHSLYTGSLWYTPIRREWYVEV IIVRVEINGQDLKMDCKEYNYDKSIV 293
 QY 246 LLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IY 305
 ||||:| | | | :|:| || :| |||| | || || |||: || |||:| | :
 Db 294 NLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLM 353
 QY 306 SRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQ 364
 :| | | | | | | | | :|:| : :| | | :| | :| | :| | | | | :| | :| |
 Db 354 NQSFRTILPQQYL RPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARK 413
 QY 365 GFAASPCAIEIAGAAVSEISGPFSTEDV 391
 ||| | | : : ||| | | :

RESULT 4

BACE_HUMAN

ID BACE_HUMAN STANDARD; PRT; 501 AA.
AC P56817; Q9BYB9; Q9BYC0; Q9BYC1; Q9UJT5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-secretase precursor (EC 3.4.23.46) (Beta-site APP cleaving
DE enzyme) (Beta-site amyloid precursor protein cleaving enzyme)
DE (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
DE protease 2) (Memapsin-2).
GN BACE OR BACE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=20002972; PubMed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Citron M.;
RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT the transmembrane aspartic protease BACE.";
RL Science 286:735-741(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND
RP CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20057171; PubMed=10591214;
RA Sinha S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,
RA Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,
RA Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
RA Tatsuno G., Tung J., Schenk D., Seubert P., Suomensaaari S.M., Wang S.,
RA Walker D., Zhao J., McConlogue L., Varghese J.;
RT "Purification and cloning of amyloid precursor protein beta-secretase
RT from human brain.";
RL Nature 402:537-540(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrichson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
RT secretase activity.";
RL Nature 402:533-537(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20120043; PubMed=10656250;
RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,

RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
 RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
 RT secretase.";
 RL Mol. Cell. Neurosci. 14:419-427(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC TISSUE=Brain, and Pancreas;
 RA Michel B., De Pietri Tonelli D., Zacchetti D., Keller P.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
 RT human brain and pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Pancreas;
 RA Zacchetti D., De Pietri Tonelli D., Schnurbus R.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
 RT human pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
 RC TISSUE=Brain;
 RX MEDLINE=21408467; PubMed=11516562;
 RA Tanahashi H., Tabira T.;
 RT "Three novel alternatively spliced isoforms of the human beta-site
 RT amyloid precursor protein cleaving enzyme (BACE) and their effect on
 RT amyloid beta-peptide production.";
 RL Neurosci. Lett. 307:9-12(2001).
 RN [8]
 RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
 RX MEDLINE=20144060; PubMed=10677483;
 RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
 RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
 RT beta-amyloid precursor protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=21950860; PubMed=11953458;
 RA Fischer F., Molinari M., Bodendorf U., Paganetti P.;
 RT "The disulphide bonds in the catalytic domain of BACE are critical but
 RT not essential for amyloid precursor protein processing activity.";
 RL J. Neurochem. 80:1079-1088(2002).
 CC -!- FUNCTION: Responsible for the proteolytic processing of the
 CC amyloid precursor protein (APP). Cleaves at the amino terminus of
 CC the A-beta peptide sequence, between residues 671 and 672 of APP,
 CC leads to the generation and extracellular release of beta-cleaved
 CC soluble APP, and a corresponding cell-associated carboxy-terminal
 CC fragment which is later release by gamma-secretase.
 CC -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=A; Synonyms=BACE-1A, BAC-501;
 CC IsoId=P56817-1; Sequence=Displayed;
 CC Name=B; Synonyms=BACE-1B, BACE-I-476;

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CC      IsoId=P56817-2; Sequence=VSP_005223;
CC      Name=C; Synonyms=BACE-1C, BACE-I-457;
CC      IsoId=P56817-3; Sequence=VSP_005222;
CC      Name=D; Synonyms=BACE-1D, BACE-I-432;
CC      IsoId=P56817-4; Sequence=VSP_005222, VSP_005223;
CC      -!- TISSUE SPECIFICITY: Brain.
CC      -!- SIMILARITY: Belongs to peptidase family A1.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF190725; AAF04142.1; -.
DR      EMBL; AF201468; AAF18982.1; -.
DR      EMBL; AF200343; AAF17079.1; -.
DR      EMBL; AF204943; AAF26367.1; -.
DR      EMBL; AF338816; AAK38374.1; -.
DR      EMBL; AF338817; AAK38375.1; -.
DR      EMBL; AB050436; BAB40931.1; -.
DR      EMBL; AB050437; BAB40932.1; -.
DR      EMBL; AB050438; BAB40933.1; -.
DR      EMBL; AF200193; AAF13715.1; -.
DR      PIR; A59090; A59090.
DR      PDB; 1M4H; 28-AUG-02.
DR      MEROPS; A01.004; -.
DR      Genew; HGNC:933; BACE.
DR      MIM; 604252; -.
DR      GO; GO:0005887; C:integral to plasma membrane; TAS.
DR      GO; GO:0008798; F:beta-aspartyl-peptidase activity; TAS.
DR      GO; GO:0009405; P:pathogenesis; TAS.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR      InterPro; IPR001969; Aspprotease_AS.
DR      InterPro; IPR009007; Pept_A_acid.
DR      InterPro; IPR001461; Peptidase_A1.
DR      Pfam; PF00026; asp; 1.
DR      PRINTS; PR00792; PEPSIN.
DR      PROSITE; PS00141; ASP_PROTEASE; 1.
KW      Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
KW      Signal; Alternative splicing; 3D-structure.
FT      SIGNAL          1          21          POTENTIAL.
FT      PROPEP          22          45
FT      CHAIN           46          501          BETA-SECRETASE.
FT      DOMAIN          22          457          EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        458          478          POTENTIAL.
FT      DOMAIN          479          501          CYTOPLASMIC (POTENTIAL).
FT      ACT_SITE        93          93          BY SIMILARITY.
FT      ACT_SITE        289         289          BY SIMILARITY.
FT      DISULFID        216         420
FT      DISULFID        278         443
FT      DISULFID        330         380
FT      CARBOHYD        153         153          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        172         172          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        223         223          N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT	CARBOHYD	354	354	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	146	189	Missing (in isoform C and isoform D).
FT				/FTId=VSP_005222.
FT	VARSPPLIC	190	214	Missing (in isoform B and isoform D).
FT				/FTId=VSP_005223.
SQ	SEQUENCE	501 AA;	55763 MW;	377CE4C824ACEF05 CRC64;

QY	9	PAGAAFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYF	68
		: : : : : : : :	
Db	54	PGRRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILVDTGSSNFAVGAAPHPFLHRY	113
QY	69	DTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENFPLPG	128
		: : : : : :	
Db	114	QRQLSSTYRDLRKGVPYPTQGWEGELGTDLVSIPHGPVNTVRANIAAITESDKFFING	173
QY	129	IKWNGILGLAYATLAKPSSSLETFDFSLVTQANIPNVFSMQMCGAGLPVAGS---GTNGG	185
		: : : : : : : : :	
Db	174	SNWEGILGLAYAEIARPDDSLEPFFDSLQTHVPNLFSLQLCGAGFPLNQSEVLASVGG	233
QY	186	SLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTT	245
		: : : : : : : : :	
Db	234	SMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGT	293
QY	246	LLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISILYLRDENS	305
		: : : : : : :	
Db	294	NLRLPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVT	353
QY	306	SRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRV	364
		: : : : : : : : : : : : : : : : :	
Db	354	NQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRI	413
QY	365	GFAASPCAEIAGAAVSEISGPFSTEDV	391
		: : :	
Db	414	GFAVSACHVHDEFRTAAVEGPFVTLDM	440

RESULT 5

```

ID      PEPC_MACFU          STANDARD;          PRT;    377 AA.
AC      P03955;
DT      23-OCT-1986 (Rel. 02, Created)
DT      01-AUG-1992 (Rel. 23, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C) (Fragment).
GN      PGC.
OS      Macaca fuscata fuscata (Japanese macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9543;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Gastric mucosa;

```

RX MEDLINE=92037645; PubMed=1935977;
 RA Kageyama T., Tanabe K., Koiwai O.;
 RT "Development-dependent expression of isozymogens of monkey
 RT pepsinogens and structural differences between them.";
 RL Eur. J. Biochem. 202:205-215(1991).
 RN [2]
 RP SEQUENCE OF 6-377.
 RX MEDLINE=86168133; PubMed=3514597;
 RA Kageyama T., Takahashi K.;
 RT "The complete amino acid sequence of monkey progastricsin.";
 RL J. Biol. Chem. 261:4406-4419(1986).
 RN [3]
 RP SEQUENCE OF 6-65.
 RX MEDLINE=85289106; PubMed=3928607;
 RA Kageyama T., Takahashi K.;
 RT "Monkey pepsinogens and pepsins. VII. Analysis of the activation
 RT process and determination of the NH2-terminal 60-residue sequence of
 RT Japanese monkey progastricsin, and molecular evolution of
 RT pepsinogens.";
 RL J. Biochem. 97:1235-1246(1985).
 CC -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
 CC shows preferential cleavage at Tyr-Xaa bonds; high activity
 CC towards hemoglobin as substrate.
 CC -!- PTM: Each pepsinogen is converted to corresponding pepsin at pH
 CC 2.0 in part as a result of the release of a 47 aa activation
 CC segment and in part as a result of stepwise proteolytic cleavage
 CC via an intermediate form(s).
 CC -!- MISCELLANEOUS: The expression of pepsinogen genes is regulated by
 CC hormones and related substances.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; X59754; CAA42426.1; -.
 DR PIR; S19683; PEMQCJ.
 DR HSSP; P20142; 1AVF.
 DR MEROPS; A01.003; -.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 5
 FT PROPEP 6 31 ACTIVATION PEPTIDE.
 FT PROPEP 32 48 ACTIVATION PEPTIDE.
 FT CHAIN 49 377 GASTRICSIN.
 FT DISULFID 93 98
 FT DISULFID 256 260

FT DISULFID 299 332
 FT ACT_SITE 80 80
 FT ACT_SITE 265 265
 FT CONFLICT 331 331 Y -> V (IN REF. 2).
 FT CONFLICT 349 349 L -> LVY (IN REF. 2).
 SQ SEQUENCE 377 AA; 41148 MW; 2CFB8F8BF26D77CE CRC64;

Query Match 17.0%; Score 359.5; DB 1; Length 377;
 Best Local Similarity 30.1%; Pred. No. 4.1e-20;
 Matches 112; Conservative 60; Mismatches 111; Indels 89; Gaps 17;

QY	30	YYLEMLIGTPPQKLQILVDTGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGF	81
		: : :	
Db	62	YFGEISIGTPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHS----RFNPSESSTYSTNGQ	117
QY	82	DVTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATIFESENFPLPG-----IKWNGILG	136
		::: : :	
Db	118	TFSLQYGSGLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMG	170
QY	137	LAYATLAKPSSSLETFFDSLVTQANIPN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPS	195
		: : : : : : :	
Db	171	LAYPTLSVDGAT--TAMQGMVQEGALTSPIFSVYLSAQ-----QGSSGGAVVFGVDSS	222
QY	196	LYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLLRLPQKVFD	255
		:: : : :: :	
Db	223	LYTGQIYWAPVTQELYWQIGIEEFLIGGQASGW-CSE--GCQAIVDTGTSLLTVPQQYMS	279
QY	256	AVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYF-----PKISYLRDENS	305
		::: :: : : :	
Db	280	ALLQA-----TGAQ-----EDEYQQLVNCNSIQNLPTLTFII-----	312
QY	306	SRSFRITILPQLYIQPMGAGLNYECY-RFGISP-----STNALVIGATVMEGFYVIF	357
		: :	
Db	313	-NGVEFPLPPSSYI-----LNNNGYCTVGVEPTYLSAQNSQPLWILGDVFLRSYYSVY	364
QY	358	DRAQKRVGFAAS	369
		: :	
Db	365	DLSNNRVGFATA	376

RESULT 6

PEPC_CALJA

ID PEPC_CALJA STANDARD; PRT; 388 AA.
 AC Q9N2D3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
 GN PGC.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 OC Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 17-26, FUNCTION, AND ENZYME
 RP REGULATION.

RC TISSUE=Gastric mucosa;
 RX MEDLINE=20250834; PubMed=10788784;
 RA Kageyama T.;
 RT "New World monkey pepsinogens A and C, and prochymosins. Purification,
 RT characterization of enzymatic properties, cDNA cloning, and molecular
 RT evolution.";
 RL J. Biochem. 127:761-770(2000).
 CC -!- FUNCTION: Hydrolyzes a variety of proteins.
 CC -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
 CC shows preferential cleavage at Tyr-Xaa bonds; high activity
 CC towards hemoglobin as substrate.
 CC -!- ENZYME REGULATION: Inhibited by pepstatin.
 CC -!- MISCELLANEOUS: The optimal pH is around 2.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; AB038385; BAA90872.1; -.
 DR PIR; JC7246; JC7246.
 DR HSSP; P20142; 1AVF.
 DR MEROPS; A01.003; -.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 59 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 60 388 GASTRICSIN.
 FT ACT_SITE 91 91 BY SIMILARITY.
 FT ACT_SITE 276 276 BY SIMILARITY.
 FT DISULFID 104 109 BY SIMILARITY.
 FT DISULFID 267 271 BY SIMILARITY.
 FT DISULFID 310 343 BY SIMILARITY.
 SQ SEQUENCE 388 AA; 42503 MW; 0BC48DBD1F7D2D8C CRC64;

Query Match 16.6%; Score 351.5; DB 1; Length 388;
 Best Local Similarity 30.1%; Pred. No. 1.7e-19;
 Matches 112; Conservative 56; Mismatches 115; Indels 89; Gaps 17;

QY 30 YYLEMLIGTPPQKLQILVDTGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGF 81
 |: |: ||||| :| ||||| | | | | | : | ||| | |
 Db 73 YFGEISIGTPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHS----RFNPSASSTYSSNGQ 128
 QY 82 DVTVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIATIFESENFFLPG-----IKWNGILG 136
 :::| || ||| | | :|: | | || | | ::||:|
 Db 129 TFSLQYGSGLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFBVYAQFDGIMG 181
 QY 137 LAYATLAKPSSSLETFFDSLVTQANIPN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPS 195

```

      ||| | :  :: |  :: :  : : ||| :  ::||::: ||:: |
Db      182 LAYPALSMGGAT--TAMQGMLQEGALTSPVFSFYLSNQ-----QGSSGGAVIFGGVDSS 233
QY      196 LYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTLLRLPQKVFD 255
      || | | :: | : :| | :|| | :  ||| :  | |  : ||| : || : || : || :
Db      234 LYTGQIYWAPVTQELYWQIGIEEFLIGGQASGW-CSE--GCQAIVDGTGTSLLTVPQQYMS 290
QY      256 AVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYF-----PKISIIYLRDENS 305
      | :||  ||:|  | : |  | :: :
Db      291 AFLEA-----TGAQ-----EDEYGGQFLVNCDSIQNLPTLTFTII----- 323
QY      306 SRSFRITILPQLYIQPMMGAGLNYECY-RFGISP-----STNALVIGATVMEGFYVIF 357
      : | ||  | : |  | : |  | ::|  : :| :|
Db      324 -NGVEFPLPPSSYI-----LSNNGYCTVGVEPTYLSSQNSQPLWILGDVFLRSYYSVF 375
QY      358 DRAQKRVGFAAS 369
      |  |||| :
Db      376 DLGNNRVGFATA 387

```

RESULT 7

PEPC_HUMAN

```

ID      PEPC_HUMAN      STANDARD;      PRT;      388 AA.
AC      P20142;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
GN      PGC.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88087276; PubMed=3335549;
RA      Hayano T., Sogawa K., Ichihara Y., Fujii-Kuriyama Y., Takahashi K.;
RT      "Primary structure of human pepsinogen C gene.";
RL      J. Biol. Chem. 263:1382-1385(1988).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89079679; PubMed=2909526;
RA      Taggart R.T., Cass L.G., Mohandas T.K., Derby P., Barr P.J., Pals G.,
RA      Bell G.I.;
RT      "Human pepsinogen C (progastricsin). Isolation of cDNA clones,
RT      localization to chromosome 6, and sequence homology with pepsinogen
RT      A.";
RL      J. Biol. Chem. 264:375-379(1989).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;
RX      MEDLINE=89290840; PubMed=2567697;
RA      Pals G., Azuma T., Mohandas T.K., Bell G.I., Bacon J.,
RA      Samloff I.M., Walz D.A., Barr P.J., Taggart R.T.;
RT      "Human pepsinogen C (progastricsin) polymorphism: evidence for a
RT      single locus located at 6p21.1-pter.";
RL      Genomics 4:137-148(1989).

```


RN [4]
 RP SEQUENCE FROM N.A.
 RA Wong R.N.S., Tang J.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE OF 17-101.
 RX MEDLINE=90130402; PubMed=2515193;
 RA Athauda S.B.P., Tanji M., Kageyama T., Takahashi K.;
 RT "A comparative study on the NH2-terminal amino acid sequences and
 RT some other properties of six isozymic forms of human pepsinogens and
 RT pepsins.";
 RL J. Biochem. 106:920-927(1989).
 RN [6]
 RP SEQUENCE OF 17-64.
 RX MEDLINE=83079318; PubMed=6816595;
 RA Foltmann B., Jensen A.L.;
 RT "Human progastricsin. Analysis of intermediates during activation
 RT into gastricsin and determination of the amino acid sequence of the
 RT propart.";
 RL Eur. J. Biochem. 128:63-70(1982).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.62 ANGSTROMS).
 RX MEDLINE=95230687; PubMed=7714902;
 RA Moore S.A., Sielecki A.R., Chernaia M.M., Tarasova N.I., James M.N.G.;
 RT "Crystal and molecular structures of human progastricsin at 1.62-A
 RT resolution.";
 RL J. Mol. Biol. 247:466-485(1995).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.36 ANGSTROMS).
 RX MEDLINE=98069649; PubMed=9406551;
 RA Khan A.R., Cherney M.M., Tarasova N.I., James M.N.;
 RT "Structural characterization of activation 'intermediate 2' on the
 RT pathway to human gastricsin.";
 RL Nat. Struct. Biol. 4:1010-1015(1997).
 CC -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
 CC shows preferential cleavage at Tyr-|-Xaa bonds; high activity
 CC towards hemoglobin as substrate.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; M18667; AAA60062.1; ALT_INIT.
 DR EMBL; M18659; AAA60062.1; JOINED.
 DR EMBL; M18660; AAA60062.1; JOINED.
 DR EMBL; M18661; AAA60062.1; JOINED.
 DR EMBL; M18662; AAA60062.1; JOINED.
 DR EMBL; M18663; AAA60062.1; JOINED.
 DR EMBL; M18664; AAA60062.1; JOINED.
 DR EMBL; M18665; AAA60062.1; JOINED.
 DR EMBL; M18666; AAA60062.1; JOINED.
 DR EMBL; M23077; AAA60063.1; -.

DR EMBL; M23069; AAA60063.1; JOINED.
 DR EMBL; M23070; AAA60063.1; JOINED.
 DR EMBL; M23071; AAA60063.1; JOINED.
 DR EMBL; M23072; AAA60063.1; JOINED.
 DR EMBL; M23073; AAA60063.1; JOINED.
 DR EMBL; M23074; AAA60063.1; JOINED.
 DR EMBL; M23075; AAA60063.1; JOINED.
 DR EMBL; J04443; AAA60074.1; -.
 DR EMBL; U75272; AAB18273.1; -.
 DR PIR; A29937; A29937.
 DR PDB; 1HTR; 26-JAN-95.
 DR PDB; 1AVF; 25-FEB-98.
 DR MEROPS; A01.003; -.
 DR Genew; HGNC:8890; PGC.
 DR MIM; 169740; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; TAS.
 DR GO; GO:0007586; P:digestion; TAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal;
 KW 3D-structure.

FT	SIGNAL	1	16	
FT	PROPEP	17	59	ACTIVATION PEPTIDE.
FT	CHAIN	60	388	GASTRICSIN.
FT	ACT_SITE	91	91	
FT	ACT_SITE	276	276	
FT	DISULFID	104	109	
FT	DISULFID	267	271	
FT	DISULFID	310	343	
FT	CONFLICT	40	41	GE -> ED (IN REF. 6).
FT	CONFLICT	52	52	W -> S (IN REF. 6).
FT	STRAND	19	25	
FT	HELIX	29	35	
FT	TURN	36	37	
FT	HELIX	39	43	
FT	TURN	44	45	
FT	HELIX	50	54	
FT	HELIX	65	68	
FT	TURN	69	70	
FT	STRAND	73	79	
FT	TURN	80	83	
FT	STRAND	84	91	
FT	TURN	92	93	
FT	STRAND	97	101	
FT	TURN	102	103	
FT	HELIX	107	110	
FT	TURN	111	111	
FT	STRAND	115	115	
FT	HELIX	117	119	
FT	TURN	121	122	
FT	STRAND	124	134	

FT	TURN	135	136
FT	STRAND	137	150
FT	TURN	151	152
FT	STRAND	153	163
FT	HELIX	169	173
FT	STRAND	178	181
FT	TURN	190	191
FT	HELIX	195	201
FT	TURN	202	203
FT	STRAND	209	214
FT	STRAND	221	227
FT	HELIX	232	234
FT	STRAND	235	244
FT	STRAND	251	254
FT	STRAND	256	259
FT	TURN	260	261
FT	STRAND	262	263
FT	TURN	266	269
FT	STRAND	271	275
FT	TURN	277	278
FT	STRAND	282	285
FT	HELIX	286	288
FT	HELIX	289	296
FT	TURN	297	297
FT	STRAND	299	300
FT	TURN	302	303
FT	STRAND	306	308
FT	HELIX	310	315
FT	STRAND	319	323
FT	TURN	324	325
FT	STRAND	326	330
FT	HELIX	332	335
FT	STRAND	336	338
FT	STRAND	343	345
FT	STRAND	347	350
FT	TURN	355	356
FT	STRAND	360	363
FT	HELIX	365	368
FT	TURN	369	370
FT	STRAND	371	376
FT	TURN	377	380
FT	STRAND	381	388
SQ	SEQUENCE	388 AA;	42426 MW; F862DFDC1438BB92 CRC64;

Query Match 16.6%; Score 350.5; DB 1; Length 388;
 Best Local Similarity 30.1%; Pred. No. 2.1e-19;
 Matches 112; Conservative 59; Mismatches 112; Indels 89; Gaps 18;

Qy	30	YYLEMLIGTPPQKLQILVDTGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGF	81
		: : : : :	
Db	73	YFGEISIGTPPQNFLVLFD TGSSNLWVPSVYCQSQACTSHS----RFPSESSTYSTNGQ	128
Qy	82	DVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENFFLPG-----IKWNGILG	136
		::: : : :: :	
Db	129	TFSLQYGSGLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNEFVYAQFDGIMG	181
Qy	137	LAYATLAKPSSSLETFFDSLVTQANIPN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPS	195

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      |||  | :  ::  |  :| :  : : ||| :  |  ::||::| ||::  |
Db      182 LAYPALSVDEAT--TAMQGMVQEGALTSPVFSVYLSNQ-----QGSSGGAVVFGGVDSS 233
QY      196 LYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLLRLPQKVFD 255
      || | |:: | : :| |::| | :  ||| :  | |  :|||:|::| | :|| :
Db      234 LYTGQIYWAPVTQELYWQIGIEEFLIGGQASGW-CSE--GCQAIVDTGTSLLTVPQQYMS 290
QY      256 AVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYF-----PKISIIYLRDENS 305
      |:::|  ||:|  | :  |  | ::  :
Db      291 ALLQA-----TGAQ-----EDEYGGQFLVNCNSIQNLPSLTFTII----- 323
QY      306 SRSFRITILPQLYIQPMMGAGLNYECY-RFGISP----STNA---LVIGATVMEGFYVIF 357
      : |  ||  | :  |  | :  |  |  ::|  :  :| : :
Db      324 -NGVEFPLPPSSYI-----LSNNGYCTVGVEPTYLSSQNGQPLWILGDVFLRSYYSVY 375
QY      358 DRAQKRVGFAAS 369
      |  |||| :
Db      376 DLGNNRVGFATA 387

```

RESULT 8

PEPC_CAVPO

```

ID      PEPC_CAVPO          STANDARD;          PRT;    394 AA.
AC      Q64411;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
GN      PGC.
OS      Cavia porcellus (Guinea pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX      NCBI_TaxID=10141;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92355614; PubMed=1644829;
RA      Kageyama T., Ichinose M., Tsukada S., Miki K., Kurokawa K., Koiwai O.,
RA      Tanji M., Yakabe E., Athauda S.B., Takahashi K.;
RT      "Gastric procathepsin E and progastricsin from guinea pig.
RT      Purification, molecular cloning of cDNAs, and characterization of
RT      enzymatic properties, with special reference to procathepsin E.";
RL      J. Biol. Chem. 267:16450-16459(1992).
CC      -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
CC      shows preferential cleavage at Tyr-|-Xaa bonds; high activity
CC      towards hemoglobin as substrate.
CC      -!- SIMILARITY: Belongs to peptidase family A1.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M88652; AAA37053.1; -.
DR      PIR; B43356; B43356.

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DR HSSP; P20142; 1AVF.
 DR MEROPS; A01.003; -.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT PROPEP 17 65 ACTIVATION PEPTIDE.
 FT CHAIN 66 394 GASTRICSIN.
 FT ACT_SITE 97 97 BY SIMILARITY.
 FT ACT_SITE 283 283 BY SIMILARITY.
 FT DISULFID 110 115 BY SIMILARITY.
 FT DISULFID 273 277 BY SIMILARITY.
 FT DISULFID 316 349 BY SIMILARITY.
 SQ SEQUENCE 394 AA; 42995 MW; 114F08E105D49865 CRC64;

Query Match 15.4%; Score 324.5; DB 1; Length 394;
 Best Local Similarity 29.0%; Pred. No. 2e-17;
 Matches 107; Conservative 63; Mismatches 116; Indels 83; Gaps 18;

QY 30 YYLEMLIGTPPQKLQILVDTGSSNF-----AVAGTPHSYIDTYFDTERSSTYRSKGF 81
 | : : : | | | | | : | | | | | : : | | | : | | : | | | :
 Db 79 YFGQISLGTTPPQS FQVLFD TGSSNLWVPSVYCSSLACTTH----TRFNPRDSSTYVATDQ 134
 QY 82 DVTVKYTQGSWTGFVGEDLVTI-----PK-GENTSFLVNIATIFESENFFLPG-----IK 130
 : : : | | | | | | : | | | | | | | | | : | | :
 Db 135 SFSLEYGTGSLTG VFGYDTMTIQDIQVPKQEFGLS-----ETE----PGSDFVYAE 181
 QY 131 WNGILGLAYATLAKPSSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVAGS--GTNGGSL 187
 : : | | | | | | : : : | : : : : : : : : | | : : | |
 Db 182 FDGILGLGYPGLSEGGAT--TAMQGLLREGALSQSLFSVYL-----GSQQGSDEGQL 231
 QY 188 VLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLL 247
 : | | : : | | | | : : : : | : | | | | : : | | : | | : | |
 Db 232 ILGGVDESLYTGDIYWTPVTQELYWQIGIEGFLIDGSASGWCSR---GCQGIVDTGTSL 288
 QY 248 RLPQKVFD AVEAVARASLIPEFS DGFWTGSQLACWTNSETPWSYFPKISYLRDENS SR 307
 : | : : : | : : | : : : : | : : :
 Db 289 TVPSDYLSTLVQAIGAE--NEYGEYF-----VSCSSIQDLPTLTFVISGV----- 332
 QY 308 SFRITILPQLYIQP-----MMGAGLNYECYRFGISPSTN--ALVIGATVMEGFYVIFDRA 360
 : | | | : : | | | : : | : : : : | : : : : | : : | |
 Db 333 --EFPLSPSAYILSGENYCMVGLESTY-----VSPGGGEPVWILGDVFLRSYYSVYDLA 384
 QY 361 QKRVGFAAS 369
 | | | | :
 Db 385 NNRVGFATA 393

RESULT 9

PEPC_RAT

ID PEPC_RAT STANDARD; PRT; 392 AA.

AC P04073;

DT 01-NOV-1986 (Rel. 03, Created)

DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
 GN PGC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RX MEDLINE=89255508; PubMed=2722863;
 RA Ishihara T., Ichihara Y., Hayano T., Katsura I., Sogawa K.,
 RA Fujii-Kuriyama Y., Takahashi K.;
 RT "Primary structure and transcriptional regulation of rat pepsinogen C
 RT gene.";
 RL J. Biol. Chem. 264:10193-10199(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RX MEDLINE=87054020; PubMed=3780741;
 RA Ichihara Y., Sogawa K., Morohashi K., Fujii-Kuriyama Y., Takahashi K.;
 RT "Nucleotide sequence of a nearly full-length cDNA coding for
 RT pepsinogen of rat gastric mucosa.";
 RL Eur. J. Biochem. 161:7-12(1986).
 RN [3]
 RP SEQUENCE OF 16-112.
 RC STRAIN=Wistar;
 RX MEDLINE=84257697; PubMed=6743670;
 RA Arai K.M., Muto N., Tani S., Akahane K.;
 RT "The N-terminal sequence of rat pepsinogen.";
 RL Biochim. Biophys. Acta 788:256-261(1984).
 CC -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
 CC shows preferential cleavage at Tyr-Xaa bonds; high activity
 CC towards hemoglobin as substrate.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; M25993; AAA41827.1; -.
 DR EMBL; M25985; AAA41827.1; JOINED.
 DR EMBL; M25986; AAA41827.1; JOINED.
 DR EMBL; M25987; AAA41827.1; JOINED.
 DR EMBL; M25988; AAA41827.1; JOINED.
 DR EMBL; M25989; AAA41827.1; JOINED.
 DR EMBL; M25990; AAA41827.1; JOINED.
 DR EMBL; M25991; AAA41827.1; JOINED.
 DR EMBL; M25992; AAA41827.1; JOINED.
 DR EMBL; X04644; CAA28305.1; -.
 DR PIR; A33510; A24608.
 DR HSSP; P20142; 1AVF.

DR MEROPS; A01.003; -.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 62 ACTIVATION PEPTIDE.
 FT CHAIN 63 392 GASTRICSIN.
 FT ACT_SITE 94 94
 FT ACT_SITE 280 280
 FT DISULFID 107 112 BY SIMILARITY.
 FT DISULFID 270 275 BY SIMILARITY.
 FT DISULFID 314 347 BY SIMILARITY.
 FT CONFLICT 31 31 E -> Q (IN REF. 3).
 FT CONFLICT 103 103 S -> A (IN REF. 3).
 FT CONFLICT 109 109 S -> L (IN REF. 3).
 SQ SEQUENCE 392 AA; 42833 MW; 092A5EAF2783EDD1 CRC64;

Query Match 14.8%; Score 313; DB 1; Length 392;
 Best Local Similarity 29.5%; Pred. No. 1.5e-16;
 Matches 105; Conservative 56; Mismatches 139; Indels 56; Gaps 16;

Qy 30 YYLEMLIGTPPQKLQILVDTGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGF 81
 | : | : | | | | | : | | | | | | | : | : | | | : |
 Db 76 YFGEISIGTTPPQNFLVLDFTGSSNLWVSSVYCQSEACTTHA----RFNPSKSSTYYTEGQ 131
 Qy 82 DVTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFFLPG-----IKWNGILG 136
 : : : | | | | | | : : | | | | | | : : | : | : | : |
 Db 132 TFSLQYGTGSLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMG 184
 Qy 137 LAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS--GTNGGSLVLGGIEP 194
 | | | | : | | : : : | : | | | | : | | : :
 Db 185 LAYPGLS--SGGATTALQGMLGE----GALSQPLFGVYL---GSQQGSNGGQIVFGGVVDK 235
 Qy 195 SLYKGDIIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVF 254
 : | | | : | : | : | | | | | : | : | | : | : | : | :
 Db 236 NLYTGEITWVPVTQELYWQITIDDFLIGDQASGW-CSSQGC-QGIVDTGTSLLVMPAQYL 293
 Qy 255 DAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSRSFRITIL 314
 : : : : | : : | : : | : | : | : : : : : : : :
 Db 294 SELLQTIGAQE--GEYGEYF-----VSCDSVSS-----LPTLSFVL-----NGVQFPLS 335
 Qy 315 PQLY-IQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGF AAS 369
 | | | | : | : : | : : | | | : | | | |
 Db 336 PSSYIIQEDNFCMVGLESLTSESGQPLWILGDVFLRSYYAIFDMGNNKVGLATS 391

RESULT 10

CATD_CLUHA

ID CATD_CLUHA STANDARD; PRT; 396 AA.

AC Q9DEX3;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Cathepsin D precursor (EC 3.4.23.5).
 OS Clupea harengus (Atlantic herring).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
 OC Clupea.
 OX NCBI_TaxID=7950;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nielsen L.B., Stougaard P., Andersen P.S., Pedersen L.H.;
 RT "Cloning and sequence determination of herring muscle cathepsin D.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 62-82.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=21165469; PubMed=11207447;
 RA Nielsen L.B., Nielsen H.H.;
 RT "Purification and characterization of cathepsin D from herring muscle
 RT (Clupea harengus).";
 RL Comp. Biochem. Physiol. 128B:351-363(2001).
 CC -!- FUNCTION: Cathepsin D is an acid protease active in intracellular
 CC protein breakdown.
 CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
 CC that of pepsin A. Does not cleave the 4-Gln-|-His-5 bond in B
 CC chain of insulin.
 CC -!- ENZYME REGULATION: Inhibited by pepstatin.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC -!- MISCELLANEOUS: The isoelectric point is 6.8. Has optimal activity
 CC at pH 2.5 with hemoglobin as the substrate and the optimal
 CC temperature is 37 degrees Celsius.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF312364; AAG27733.1; -.
 DR HSSP; P07339; 1LYB.
 DR MEROPS; A01.009; -.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Signal; Zymogen.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 61 ACTIVATION PEPTIDE.
 FT CHAIN 62 396 CATHEPSIN D.
 FT ACT_SITE 94 94 BY SIMILARITY.
 FT ACT_SITE 281 281 BY SIMILARITY.
 FT DISULFID 107 114 BY SIMILARITY.
 FT DISULFID 272 276 BY SIMILARITY.

FT DISULFID 315 352 BY SIMILARITY.
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 396 AA; 43315 MW; D0375DC38567A31B CRC64;

Query Match 14.7%; Score 311; DB 1; Length 396;
 Best Local Similarity 28.3%; Pred. No. 2.2e-16;
 Matches 105; Conservative 59; Mismatches 125; Indels 82; Gaps 16;

Qy	30	YYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDT-----YFDTERSSTYRSKGFVDV	83
		: : : : : : :	
Db	76	YYGEIGLGTPVQMFTVVFDTGSSNLWLPSIHCSFTDIACLLHHKYNGAKSSTYVKNNGTEF	135
Qy	84	TVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFFLPGI-----KWNIGILGLA	138
		: : : : : : : : : : : :	
Db	136	AIQYGSGLSLSGYLSQDSCTI-----GDIVVEKQLF-GEAIKQPGVAFIAAKFDGILGMA	188
Qy	139	YATLAKPSSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVAGSGTN-----GGSLVLGGI	192
		: : : : : : : : :	
Db	189	YPRIS--VDGVPPVFDMMMSQKKVEQNVFSFYI-----NRNPDTEPGGELLGGT	236
Qy	193	EPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLRLPQK	252
		: : : : : : : : : : :	
Db	237	DPKYYTGDFNYVPVTRQAYWQIHMDGMSIGSQ-LTL-CKD--GCEAIVDTGTSLITGPPA	292
Qy	253	VFDAVVEAVARASLI-----PEFSDGFWTGSQACWTNSETPWSYFPKISI	298
		: : : :	
Db	293	EVRAALQKAIGAIPLIQGEYMIDCKKVPTLPTIS--FNVGGK----TYSLTGEQY-----	340
Qy	299	YLRDENSRSRFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	358
		: : : : : : : : : :	
Db	341	VLKESQGGKTICLSGLMGLEIPP-----PAGPLWILGDVFIGQYYTVFD	384
Qy	359	RAQKRVGFSAAS	369
Db	385	RESNRVGFSAKS	395

RESULT 11

PEPE_CHICK

ID PEPE_CHICK STANDARD; PRT; 383 AA.
 AC P16476;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Embryonic pepsinogen precursor (EC 3.4.23.-).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88227903; PubMed=3131317;
 RA Hayashi K., Agata K., Mochii M., Yasugi S., Eguchi G., Mizuno T.;
 RT "Molecular cloning and the nucleotide sequence of cDNA for embryonic
 RT chicken pepsinogen: phylogenetic relationship with prochymosin."
 RL J. Biochem. 103:290-296(1988).


```

CC  -!- DEVELOPMENTAL STAGE: Specifically secreted during the embryonic
CC      period in the chicken proventriculus (glandular stomach).
CC  -!- SIMILARITY: Belongs to peptidase family A1.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; D00215; BAA00153.1; -.
DR  PIR; A41443; A41443.
DR  HSSP; P00794; 4CMS.
DR  MEROPS; A01.028; -.
DR  InterPro; IPR001969; Aspprotease_AS.
DR  InterPro; IPR009007; Pept_A_acid.
DR  InterPro; IPR001461; Peptidase_A1.
DR  Pfam; PF00026; asp; 1.
DR  PRINTS; PR00792; PEPSIN.
DR  PROSITE; PS00141; ASP_PROTEASE; 2.
KW  Hydrolase; Aspartyl protease; Digestion; Signal; Glycoprotein.
FT  SIGNAL          1      16      POTENTIAL.
FT  CHAIN           17     383     EMBRYONIC PEPSINOGEN.
FT  ACT_SITE        94      94      BY SIMILARITY.
FT  ACT_SITE       276     276     BY SIMILARITY.
FT  DISULFID       107     112     BY SIMILARITY.
FT  DISULFID       267     271     BY SIMILARITY.
FT  DISULFID       310     344     BY SIMILARITY.
FT  CARBOHYD       132     132     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD       204     204     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD       309     309     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD       350     350     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  VARIANT         51      51      T -> S.
SQ  SEQUENCE      383 AA;  41719 MW;  1642796871611F54 CRC64;

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Query Match          14.5%;  Score 306.5;  DB 1;  Length 383;
Best Local Similarity 26.9%;  Pred. No. 4.6e-16;
Matches 96;  Conservative 62;  Mismatches 128;  Indels 71;  Gaps 12;

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QY      30 YYLEMLIGTPPQKLQILVDTGSSNFAVAG----TPHSYIDTYFDTERSSTYRSKGFDTV 85
      || : |||||  :: ||||| |      :|      |: :|||:| | ::::
Db      76 YYGTTISIGTPPQDFTVVFDTGSSNLWVPSVSC TSPACQSHQMFNPSQSSTYKSTGQNLSI 135

QY      86 KYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATIFESENFFLPGIKWNGILGLAYATLAKP 145
      | | | || |||:  ::| | ::| | ||: :|:||||| | :||
Db      136 HYGTDMEGTVGCDTVTVASLMDTNQLFGLST-SEPGQFFV-YVKFDGILGLGYPSLA-- 191

QY      146 SSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIIWYT 204
      : : ||::| :: : |::: :      :      | :| |||: | : | | :
Db      192 ADGITPVFDNMVNESLLEQNLF SVYLSREPM-----GSMVVFGGIDESYFTGSINWI 243

QY      205 PIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAI VDSGTTLLRLPQKVFDAVVEAVARA 264
      |: : |::| : : : | :      : :||:|:|:|:| | : : ||
Db      244 PVS YQGYWQISMDSIIVNKQEIACS----SGCQAIIDTGTSLVAGPASDINDIQSAVG-- 297

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Qy      265 SLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMG 324
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      298 -----ANQNTYGEY-----SVNCSHILAMPDVVF--VIG 324

Qy      325 AGLNY-----ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFA 367
          | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      325 -GIQYPVPALAYTEQNGQGTCMSSFQNSSADLWILGDVVFIRVYYSIFDRANNRVGLA 380

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RESULT 12

CATD_MOUSE

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ID      CATD_MOUSE      STANDARD;      PRT;      410 AA.
AC      P18242;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Cathepsin D precursor (EC 3.4.23.5).
GN      CTSD.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Brain;
RX      MEDLINE=91088345; PubMed=2263503;
RA      Diedrich J.F., Staskus K.A., Retzel E.F., Haase A.T.;
RT      "Nucleotide sequence of a cDNA encoding mouse cathepsin D.";
RL      Nucleic Acids Res. 18:7184-7184(1990).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90326544; PubMed=2374732;
RA      Grusby M.J., Mitchell S.C., Glimcher L.H.;
RT      "Molecular cloning of mouse cathepsin D.";
RL      Nucleic Acids Res. 18:4008-4008(1990).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J;
RX      MEDLINE=94280622; PubMed=8011168;
RA      Hetman M., Perschl A., Saftig P., von Figura K., Peters C.;
RT      "Mouse cathepsin D gene: molecular organization, characterization of
RT      the promoter, and chromosomal localization.";
RL      DNA Cell Biol. 13:419-427(1994).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Brain, and Mammary gland;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

```

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.
 CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
 CC that of pepsin A. Does not cleave the 4-Gln-|-His-5 bond in B
 CC chain of insulin.
 CC -!- SUBUNIT: Consists of a light chain and a heavy chain.
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; X53337; CAA37423.1; -.
 DR EMBL; X52886; CAA37067.1; -.
 DR EMBL; X68378; CAA48453.1; -.
 DR EMBL; X68379; CAA48453.1; JOINED.
 DR EMBL; X68380; CAA48453.1; JOINED.
 DR EMBL; X68381; CAA48453.1; JOINED.
 DR EMBL; X68382; CAA48453.1; JOINED.
 DR EMBL; X68383; CAA48453.1; JOINED.
 DR EMBL; BC054758; AAH54758.1; -.
 DR EMBL; BC057931; AAH57931.1; -.
 DR PIR; I48278; KHMSD.
 DR HSSP; P07339; 1LYB.
 DR MEROPS; A01.009; -.
 DR MGD; MGI:88562; Ctsd.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 64 ACTIVATION PEPTIDE (POTENTIAL).
 FT CHAIN 65 410 CATHEPSIN D.
 FT ACT_SITE 97 97 BY SIMILARITY.
 FT ACT_SITE 293 293 BY SIMILARITY.
 FT DISULFID 91 160 BY SIMILARITY.
 FT DISULFID 110 117 BY SIMILARITY.
 FT DISULFID 284 288 BY SIMILARITY.
 FT DISULFID 327 364 BY SIMILARITY.
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (BY SIMILARITY).

FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ SEQUENCE 410 AA; 44954 MW; DC4928EC46928BF0 CRC64;

Query Match 14.5%; Score 306.5; DB 1; Length 410;
Best Local Similarity 27.5%; Pred. No. 5e-16;
Matches 103; Conservative 64; Mismatches 123; Indels 85; Gaps 15;

```
Qy      30 YYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDT-----YFDTERSSTYRSKGFDV 83
      || :: ||||| :: ||||| | :| ::::| ||| |
Db      79 YYGDIGIGTPPQCFTVVFDTGSSNLWVPSIHCKILDIACWVHHKYNSDKSSTYVKNGTSF 138

Qy      84 TVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIAT---IFESENFFLPGI-----KWNIGIL 135
      : | || :|: :| |::| : | | || | || | :|: |||
Db     139 DIHYGSGSLSGYLSQDTVSVPCCKSDQSKARGIKVEKQIF-GEATKQPGIVFVAAKFDGIL 197

Qy     136 GLAYATLAKPSSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEP 194
      |: | :: :: ||:|: | : | :|| | | || | :|: |||
Db     198 GMGYPHIS--VNNVLPVFDNLMQQKLVDKNIFSFY-----LNRDPEGQPGGELMLGGTDS 250

Qy     195 SLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVF 254
      | |:| : : : |:|: : :||:| : | | |: :|||:|:| | | :
Db     251 KYYHGELSYLNVTRKAYWQVHMDQLEVGNE-LTL-CK--GGCEAIVDTGTSLLVGPVEEV 306

Qy     255 DAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIIYLRDENSSRSFRITIL 314
      : :|: || : | : :|
Db     307 KELQKAIGAVPLI-----QGEYMIPCEKVSSL 333

Qy     315 PQLYIQPMMGAGLNYEC-----YRFGIS-----PSTNALVIGATVMEG 352
      | :|: : :| | || | :| :| || :|: | :
Db     334 PTVYLK--LG-GKNYELHPDKYILKVSQGGKTICLSGFMGMDIPPPSGPLWILGDVFIGS 390

Qy     353 FYVIFDRAQKRVGFA 367
      :| :||| |||||
Db     391 YYTVFDRDNNRVGFA 405
```

RESULT 13

CATD_RAT

ID CATD_RAT STANDARD; PRT; 407 AA.
AC P24268;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5).
GN CTSD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pituitary;
RX MEDLINE=91057150; PubMed=2243802;
RA Birch N.P., Loh Y.P.;
RT "Cloning, sequence and expression of rat cathepsin D."
RL Nucleic Acids Res. 18:6445-6445(1990).
RN [2]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 65-74; 118-127 AND 165-174.
 RC TISSUE=Liver;
 RX MEDLINE=91354249; PubMed=1883350;
 RA Fujita H., Tanaka Y., Noguchi Y., Kono A., Himeno M., Kato K.;
 RT "Isolation and sequencing of a cDNA clone encoding rat liver
 RT lysosomal cathepsin D and the structure of three forms of mature
 RT enzymes.";
 RL Biochem. Biophys. Res. Commun. 179:190-196(1991).
 RN [3]
 RP SEQUENCE OF 134-170.
 RX MEDLINE=89034127; PubMed=3182800;
 RA Yonezawa S., Takahashi T., Wang X., Wong R.N.S., Hartsuck J.A.,
 RA Tang J.;
 RT "Structures at the proteolytic processing region of cathepsin D.";
 RL J. Biol. Chem. 263:16504-16511(1988).
 CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.
 CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
 CC that of pepsin A. Does not cleave the 4-Gln-|-His-5 bond in B
 CC chain of insulin.
 CC -!- SUBUNIT: Occurs as a mixture of both a single chain form and two
 CC types of two chain (light and heavy) forms.
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; X54467; CAA38349.1; -.
 DR PIR; S13111; KHRTD.
 DR HSSP; P07339; 1LYB.
 DR MEROPS; A01.009; -.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal;
 KW Lysosome.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 64 ACTIVATION PEPTIDE (POTENTIAL).
 FT CHAIN 65 407 CATHEPSIN D.
 FT CHAIN 65 164 CATHEPSIN D 12 kDa LIGHT CHAIN.
 FT CHAIN 165 407 CATHEPSIN D 30 kDa HEAVY CHAIN.
 FT CHAIN 65 117 CATHEPSIN D 9 kDa LIGHT CHAIN.
 FT CHAIN 118 407 CATHEPSIN D 34 kDa HEAVY CHAIN.
 FT ACT_SITE 97 97 BY SIMILARITY.
 FT ACT_SITE 290 290 BY SIMILARITY.
 FT DISULFID 91 160 BY SIMILARITY.
 FT DISULFID 110 117 BY SIMILARITY.
 FT DISULFID 281 285 BY SIMILARITY.
 FT DISULFID 324 361 BY SIMILARITY.

FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	258	258	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	15	15	D -> A (IN REF. 2).
FT	CONFLICT	163	163	D -> T (IN REF. 3).
FT	CONFLICT	205	205	K -> N (IN REF. 2).
FT	CONFLICT	262	262	K -> N (IN REF. 2).
SQ	SEQUENCE	407 AA;	44680 MW;	C423AD4104D95F84 CRC64;

```

QY      30 YYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDT-----YFDTERSSTYRSKGFDV 83
      || |: ||||| :: ||||| | :| ::::||| |
Db      79 YYGEIGIGTPPQCFTVVFDTGSSNLWVPSIHCKLLDIACWVHHKYNSDKSSTYVKNGTSTF 138

QY      84 TVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATIFESENFFLPGI-----KWNIGILGLA 138
      : | || :|:: :| |::| : : || | ||: |::|||:
Db     139 DIHYGSGSLSGYLSQDTVSVPCSDLGGIKVEKQIF-GEATKQPGVVFIAAKFDGILGMG 197

QY     139 YATLAKPSSSLETFDSLVTQANI-PNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLY 197
      | :: : : ||::| : |::| | :| || |::||| : |
Db     198 YPFIS--VNKVLPVFDNLMKQKLVEKNIFSFY-----LNRDPTGQPGGELMLGGTDSRY 250

QY     198 KGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAI VDSGTTLLRLPQKVFDV 257
      |:: | : : |::: : ||::| : | | |: :|||:|::|| | |
Db     251 HGELSYLNVTRKAYWQVHMDQLEVGSE-LTL-CK--GGCEAIVDTGTSLLVGP---VDEV 303

QY     258 VEAVARASLIPEFS DGFWTGSQLACWTNSETPWSYFPKIS IYLRDENS SRSFRTILPQL 317
      | :| : : | | | |: | :| : |:
Db     304 KELQKAIGAVPLIQGEY----MIPC-----EKVSSLPIITFKLGGQN-----YELHPEK 348

QY     318 YIQPMMGAGLNYECYRF---GISPSTNAL-VIGATVMEGFYVIFDRAQKRVGFA 367
      || : || | | | : |::| : :| :||| ||||
Db     349 YILKVSQAGKTICLSGFMGMDIPPPSGPLWILGDVFIGCYTTFDREYNRVGFA 402

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RESULT 14

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ID      REN1_MOUSE          STANDARD;          PRT;      402 AA.
AC      P06281; P97911; Q62153; Q62154;
DT      01-JAN-1988 (Rel. 06, Created)
DT      01-JAN-1988 (Rel. 06, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Renin 1 precursor (EC 3.4.23.15) (Angiotensinogenase) (Kidney renin).
GN      REN1 OR REN-1 OR REN.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RX      MEDLINE=84182525; PubMed=6370686;
RA      Holm I., Ollo R., Panthier J.-J., Rougeon F.;
RT      "Evolution of aspartyl proteases by gene duplication: the mouse renin
RT      gene is organized in two homologous clusters of four exons.";

```

RL EMBO J. 3:557-562(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Kidney;
 RX MEDLINE=90067953; PubMed=2685761;
 RA Kim W.S., Murakami K., Nakayama K.;
 RT "Nucleotide sequence of a cDNA coding for mouse Ren1 preprorenin.";
 RL Nucleic Acids Res. 17:9480-9480(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2, and C57BL/10;
 RX MEDLINE=90108722; PubMed=2691339;
 RA Burt D.W., Mullins L.J., George H., Smith G., Brooks J., Pioli D.,
 RA Brammar W.J.;
 RT "The nucleotide sequence of a mouse renin-encoding gene, Ren-1d, and
 RT its upstream region.";
 RL Gene 84:91-104(1989).
 RN [4]
 RP SEQUENCE OF 1-30 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=84298161; PubMed=6089205;
 RA Panthier J.-J., Dreyfus M., Roux D.T.L., Rougeon F.;
 RT "Mouse kidney and submaxillary gland renin genes differ in their 5'
 RT putative regulatory sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5489-5493(1984).
 RN [5]
 RP SEQUENCE OF 1-31 FROM N.A.
 RX MEDLINE=85085936; PubMed=6392850;
 RA Field L.J., Philbrick W.M., Howles P.N., Dickinson D.P.,
 RA McGowan R.A., Gross K.W.;
 RT "Expression of tissue-specific Ren-1 and Ren-2 genes of mice:
 RT comparative analysis of 5'-proximal flanking regions.";
 RL Mol. Cell. Biol. 4:2321-2331(1984).
 RN [6]
 RP SEQUENCE OF 22-37 AND 72-80.
 RC STRAIN=C57BL/10ROS X C3H/HEROS; TISSUE=Kidney;
 RX MEDLINE=97182599; PubMed=9030738;
 RA Jones C.A., Petrovic N., Novak E.K., Swank R.T., Sigmund C.D.,
 RA Gross K.W.;
 RT "Biosynthesis of renin in mouse kidney tumor As4.1 cells.";
 RL Eur. J. Biochem. 243:181-190(1997).
 CC -!- FUNCTION: Renin is a highly specific endopeptidase, whose only
 CC known function is to generate angiotensin I from angiotensinogen
 CC in the plasma, initiating a cascade of reactions that produce an
 CC elevation of blood pressure and increased sodium retention by the
 CC kidney.
 CC -!- CATALYTIC ACTIVITY: Cleaves Leu-|- bond in angiotensinogen to
 CC generate angiotensin I.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Kidney.
 CC -!- INDUCTION: Renal renin is synthesized by the juxtaglomerular cells
 CC of the kidney in response to decreased blood pressure and sodium
 CC concentration.
 CC -!- POLYMORPHISM: In inbred mouse strains, there are at least two
 CC alleles which can occur at the Ren1 locus: Ren-1D and Ren-1C.
 CC The sequence shown is that of Ren-1C.
 CC -!- SIMILARITY: Belongs to peptidase family A1.


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CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00810; CAA25391.1; -.
DR EMBL; X00811; CAA25391.1; JOINED.
DR EMBL; X00812; CAA25391.1; JOINED.
DR EMBL; X00813; CAA25391.1; JOINED.
DR EMBL; X00814; CAA25391.1; JOINED.
DR EMBL; X00815; CAA25391.1; JOINED.
DR EMBL; X00816; CAA25391.1; JOINED.
DR EMBL; X00850; CAA25391.1; JOINED.
DR EMBL; X00851; CAA25391.1; JOINED.
DR EMBL; X16642; CAA34636.1; -.
DR EMBL; K02596; AAA40045.1; -.
DR EMBL; M32352; AAA40043.1; -.
DR EMBL; K02800; AAA40044.1; -.
DR EMBL; M34190; AAA40042.1; -.
DR PIR; A00989; REMSK.
DR HSSP; P00796; 1SMR.
DR MEROPS; A01.007; -.
DR MGD; MGI:97898; Ren1.
DR InterPro; IPR001969; Aspprotease_AS.
DR InterPro; IPR009007; Pept_A_acid.
DR InterPro; IPR001461; Peptidase_A1.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
KW Hydrolase; Aspartyl protease; Plasma; Glycoprotein; Zymogen;
KW Signal.
FT SIGNAL 1 21
FT PROPEP 22 71 ACTIVATION PEPTIDE.
FT CHAIN 72 402 RENIN 1.
FT ACT_SITE 102 102 BY SIMILARITY.
FT ACT_SITE 287 287 BY SIMILARITY.
FT DISULFID 115 122 BY SIMILARITY.
FT DISULFID 278 282 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 58 58 W -> R (in Ren-1D).
FT VARIANT 68 68 T -> I (in Ren-1D).
FT VARIANT 160 160 S -> V (in Ren-1D).
FT VARIANT 315 315 E -> D (in Ren-1D).
FT VARIANT 352 352 N -> Y (in Ren-1D).
FT CONFLICT 6 23 MISSING (IN REF. 1).
FT CONFLICT 24 24 T -> I (IN REF. 1).
FT CONFLICT 163 163 V -> VSRV (IN REF. 1).
SQ SEQUENCE 402 AA; 44342 MW; D42920B555E97A38 CRC64;

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Query Match      14.4%; Score 304; DB 1; Length 402;
Best Local Similarity 29.0%; Pred. No. 7.6e-16;

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Matches 108; Conservative 60; Mismatches 152; Indels 52; Gaps 17;

```
Qy      6 LASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSY-- 63
      | ||      |:|      | |      || |: |||||      ::: ||||:| | | |
Db      70 LTSPVVLTNYL----NTQ-----YYGEIGIGTPPQTFKVI FDTGSANLWVPSTKCSRLY 119

Qy      64 ----IDTYFDTERSSTYRSKGFDTVYKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATIF 119
      | : ::: ||:| | | |: | | ||: :| ||: | : |
Db      120 LACGIHSLYESSDSSSYMENGSDFTIHYGSGRVKGFLSQDSVTV-GGITVTQT FGEVTEL 178

Qy      120 ESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVA 178
      | | |:::|::: : | : | |:::| : |||:
Db      179 PLIPFML--AKFDGVLGMGFP--AQAVGGVTPVFDHILSQGVLKEEVFSVYY-----NR 228

Qy      179 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 238
      || || :||| :| |:|: | | : :|| : : :| | | | |
Db      229 GSHLLGGEVVLGGSDPQHYQGNFHYVSISKTD SWQITMKGVS VG--SSTLLCEE GCA--V 284

Qy      239 IVDSGTTLLRLPQKVFD AVEAV-ARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS 297
      :||:|:: : | :::|: |: | |: : | |: | | |
Db      285 VVDTGSSSFISAPTSSLKLIMQALGAKEKRIEY-----VVNC---SQVP--TLPDIS 331

Qy      298 IYLRDENSRSRFRITILPQLYIQPMMGAGL-NYECYRFGISPSTNAL-VIGATVMEGFYV 355
      | |::: : | | : | | | : |:| | : ||
Db      332 FDL---GGRAYTLSSTDYVLQYPNRRDKLCTLALHAMDIPPTGPVWVLGATFIRKFYT 387

Qy      356 IFDRAQKRVGFA 367
      ||| |:| |
Db      388 EFDRHNNRIGFA 399
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RESULT 15

PEP1_GADMO

ID PEP1_GADMO STANDARD; PRT; 324 AA.
AC P56272;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pepsin IIB (EC 3.4.23.-).
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY.
RC TISSUE=Stomach;
RA Karlsen S., Hough E., Olsen R.L.;
RT "Structure and proposed amino-acid sequence of a pepsin from Atlantic
RT cod (Gadus morhua).";
RL Acta Crystallogr. D 54:32-46(1998).
CC -!- SIMILARITY: Belongs to peptidase family A1.
DR PDB; 1AM5; 24-DEC-97.
DR InterPro; IPR001969; Aspprotease_AS.
DR InterPro; IPR009007; Pept_A_acid.
DR InterPro; IPR001461; Peptidase_A1.
DR Pfam; PF00026; asp; 1.

DR	PRINTS; PR00792; PEPSIN.		
DR	PROSITE; PS00141; ASP_PROTEASE; 2.		
KW	Hydrolase; Aspartyl protease; Digestion; 3D-structure.		
FT	ACT_SITE	32	32 BY SIMILARITY.
FT	ACT_SITE	214	214 BY SIMILARITY.
FT	DISULFID	45	50 BY SIMILARITY.
FT	DISULFID	206	209 BY SIMILARITY.
FT	DISULFID	247	280 BY SIMILARITY.
FT	STRAND	2	9
FT	TURN	10	12
FT	STRAND	13	20
FT	TURN	21	24
FT	STRAND	25	32
FT	TURN	33	34
FT	STRAND	38	40
FT	STRAND	42	42
FT	TURN	43	44
FT	HELIX	48	51
FT	TURN	52	52
FT	STRAND	56	56
FT	HELIX	58	60
FT	TURN	62	63
FT	STRAND	65	74
FT	STRAND	79	90
FT	STRAND	96	106
FT	TURN	110	114
FT	STRAND	119	122
FT	HELIX	126	128
FT	HELIX	130	132
FT	HELIX	136	142
FT	TURN	143	144
FT	STRAND	150	154
FT	TURN	158	159
FT	STRAND	163	167
FT	HELIX	172	174
FT	STRAND	175	175
FT	STRAND	180	187
FT	TURN	188	189
FT	STRAND	190	194
FT	STRAND	196	199
FT	TURN	200	201
FT	STRAND	202	203
FT	STRAND	209	213
FT	TURN	215	216
FT	STRAND	220	222
FT	TURN	224	226
FT	HELIX	227	234
FT	TURN	235	235
FT	STRAND	237	238
FT	STRAND	243	244
FT	TURN	247	248
FT	STRAND	256	260
FT	TURN	261	262
FT	STRAND	263	267
FT	HELIX	269	272
FT	STRAND	273	275
FT	STRAND	280	282

FT STRAND 284 286
 FT STRAND 296 299
 FT HELIX 301 306
 FT STRAND 307 312
 FT TURN 313 316
 FT STRAND 317 324
 SQ SEQUENCE 324 AA; 34014 MW; EE3A6097B6941DD7 CRC64;

Query Match 14.3%; Score 302; DB 1; Length 324;
 Best Local Similarity 25.6%; Pred. No. 8.1e-16;
 Matches 94; Conservative 75; Mismatches 134; Indels 64; Gaps 15;

Qy	18	MVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNF-----AVAGTPHSYIDTYFD	69
		: : : : : : : : : : : :	
Db	2	VTEQMKNEADTEYYGVISIGTPPESFKVIFDTGSSNLWVSSSHCSAQACSNHN----KFK	57
Qy	70	TERSSTYRSKGFDTVKYTGQSWTGFGEDLVTPKGFNTSFLVNIATIFESENF---FL	126
		: : : : : : : : : : :	
Db	58	PRQSSTYVETGKTVDLTYGTGGMRGILGQDTVSVGGGSDPN-----QELGESQTEPGPFQ	112
Qy	127	PGIKWNGILGLAYATLAKPSSSLETFFDLSVTQANI-PNVFSMQMCGAGLPVAGSGTNGG	185
		: : : : : : : : : : : :	
Db	113	AAAPFDGILGLAYPSIA--AAGAVPVFDNMGSQSLVEKDLFSFYL-----SGGGANGS	163
Qy	186	SLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD-CREYNADKAIVDSGT	244
		: : : : : : : : : : : : : :	
Db	164	EVMLGGVDNSHYTGSIHWIPVTAEKYWQVALDGITVNGQTAACEGC-----QAIVDTGT	217
Qy	245	TLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDEN	304
		: : : : : : : : : : : :	
Db	218	SKIVAPVSALANIMKDIGASE-----NQGEMMGN---CASVQSLPDITF-----	258
Qy	305	SSRSFRITILPQLYI---QPMMGAGLNYECYRFGISPSTNAL-VIGATVMEGFYVIFDRA	360
		: : : : : : : : : : :	
Db	259	TINGVKQPLPPSAYIEGDQAFCTSGLGSS----GVPSNTSELWIFGDVFLRNYTYTIYDRT	314
Qy	361	QKRVGFA	367
		:	
Db	315	NNKVGFA	321

Search completed: March 4, 2004, 15:36:25
 Job time : 13.9574 secs